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Om protein - protein search, using sw model  
Run on: January 21, 2005, 08:04:52 ; Search time 83 SecondB  
69.153 Million cell updates/sec

Title: US-09-845-765-1  
Perfect score: 83  
Sequence: 1 ADSGEGDFLAEGGVVR 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Genesed\_23Seq04:  
1: geneseqP1990s:  
2: geneseqP1990s:  
3: geneseqP2000s:  
4: geneseqP2001s:  
5: geneseqP2002s:  
6: geneseqP2003as:  
7: geneseqP2003bs:  
8: geneseqP2004s:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	83	100.0	16 2	AAB96194 Fibronage
2	83	100.0	16 2	AAW04619 Fibronope
3	83	100.0	16 2	AYV57487 Antimicro
4	83	100.0	16 4	ABBS5621 Vascular
5	83	100.0	16 4	AAB91959 Fibronect
6	83	100.0	16 4	ABP52337 Human API
7	83	100.0	16 5	ABG73668 Linear HI
8	83	100.0	16 5	ABG78799 Multiple
9	83	100.0	16 5	ABG70000 Antimicro
10	83	100.0	16 5	ABG69911 Rabbit Pl
11	83	100.0	16 6	ABP60019 Biopolymer
12	83	100.0	16 6	ABP60640 Fibronope
13	83	100.0	16 6	ADL18542 Human alp
14	83	100.0	16 6	ABR58740 Alzheimer
15	83	100.0	16 7	ADF51340 Antiangi
16	83	100.0	16 7	ADP41579 Human fib
17	83	100.0	16 8	ADF90108 Human fib
18	83	100.0	16 8	ADN3162 Human Alz
19	83	100.0	16 8	ADQ96599 Human alp
20	83	100.0	17 4	ABR91960 Fibronect
21	83	100.0	17 6	ABD08833 Alpha fib
22	83	100.0	17 6	ABD90101 Alpha fib
23	83	100.0	17 8	ADG93163 Novel exp
24	83	100.0	17 8	ADJ65841 Fibrinope
25	83	100.0	17 8	ADN03327 Exemplary

RESULT 1	
ID	AAB96194 standard; peptide; 16 AA.
XX	
AC	AAB96194;
XX	
DT	19-DEC-1996 (first entry)
DE	Fibrinogen epitope probe, represents alpha chain residues 1-16.
XX	
EPITOPE; CLEAVAGE PRODUCT; HUMAN; LEUKOCYTE ELASTASE; HLE; FIBRINOGEN; MONOCLONAL ANTIBODY; PROBE; DETECTION; ANTIGEN; BLOOD; PERITONEAL FLUID; BUTYRUM; BRONCHIAL ALVEOLAR LAVAGE FLUID; ASSAY; INHIBITOR; ARTHRITIS; PULMONARY EMPHYSEMA; CHRONIC BRONCHITIS; CYSTIC FIBROSIS; BRONCHIECTASIS; INFANTILE RESPIRATORY DISTRESS SYNDROME; MYELOGENOUS LEUKAEMIA; ADULT RESPIRATORY DISTRESS SYNDROME.	
KW	
XX	
OS	Homo sapiens.
XX	
PN	W09614580-A1.
XX	
PD	17-MAY-1996.
XX	
PP	03-NOV-1995; 95WO-US013794.
XX	
PR	07-NOV-1994; 94US-0033524.
PR	06-JUN-1995; 95US-00469141.
XX	
PA	(MERI ) MERCK & CO INC.
XX	
PT	Munford RA, Davies DTP, Dahlgren ME, Boger JS, Humes JL,
XX	
DR	WPI; 1996-251888/25.
XX	
PT	New isolated fibrinogen derived cleavage products - used for detection of leukocyte elastase activity in disease diagnosis and for evaluating elastase inhibitors.
XX	
PS	Example 5; Page 42; 109pp; English.
XX	
CC	The sequences given in AB96192-94 represent antigenic probes derived from the first 21 amino acids of human fibrinogen. These probes are used to determine antibody titer against other fibrinogen cleavage products.
CC	The monospecific antibodies may be used to assay for the formation of complementary cleavage product antigens or epitopes in whole blood or other body fluids, peritoneal fluid, sputum or bronchial alveolar lavage fluid. The assay for cleavage products is dependent upon the presence of

CC HLB in the sample. This assay can also be used for the evaluation of HLB  
 CC inhibitors. The antibodies may be used to diagnose and monitor disease  
 CC such as arthritis, gout, pulmonary emphysema, chronic bronchitis, cystic  
 CC fibrosis, chronic obstructive pulmonary disease, bronchiectasis, adult or  
 CC infantile respiratory distress syndrome and myelogenous leukaemia. See  
 CC also AAR96146-81

XX SQ Sequence 16 AA;

RESULT 2

Query Match	100.0%	Score	83;	DB	2;	Length	16;			
Best Local Similarity	100.0%	Pred.	No.	1.3e-05;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	16;	Conservative	0;							

OY 1 ADSGEGRPLAEGGGVR 16  
 Db 1 ADSGEGRPLAEGGGVR 16

RESULT 3

Query Match	100.0%	Score	83;	DB	2;	Length	16;			
Best Local Similarity	100.0%	Pred.	No.	1.3e-05;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	16;	Conservative	0;							

OY 1 ADSGEGRPLAEGGGVR 16  
 Db 1 ADSGEGRPLAEGGGVR 16

RESULT 4

Query Match	100.0%	Score	83;	DB	2;	Length	16;			
Best Local Similarity	100.0%	Pred.	No.	1.3e-05;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	16;	Conservative	0;							

OY 1 ADSGEGRPLAEGGGVR 16  
 Db 1 ADSGEGRPLAEGGGVR 16

Db 1 |||||||ADSGEGRPLAEGGGVR 16

XX ID AAY57487 standard; peptide, 16 AA.

XX AC AAY57487;

XX DT 25-FEB-2000 (first entry)

DB Antimicrobial peptide CS-FBP-alpha SEQ ID NO:25.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;

XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.

OS Oryctolagus cuniculus.

PN WO9942119-A1.

XX DR 1999-02-23.

XX PD 26-AUG-1999.

XX PP 17-FEB-1999; 99WO-US003350.

XX PR 18-FEB-1998; 98US-00023319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 1999-527417/44.

XX PT Antimicrobial peptides for potentiating antimicrobial agents active  
 PT against bacteria and fungi.

XX PS Disclosure; Page 120; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XZBZXBXB and its derivatives  
 CC selected from XZBZXBXB, BXZXB, BXZXZXB, XBXZXB and BXZBZXB; and (b)  
 CC a second peptide template XBZBX and their derivatives selected from the  
 CC group consisting of XBBXB, XBBXXB, BXXBXB, XBZXXB, and  
 CC XBBZXBZXBZXB, where B = at least one positively charged amino acid; Z =  
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic  
 CC amino acid, and where B, X and Z may be separated by one or more other  
 CC amino acids. The peptides can be used to treat bacterial and fungal  
 CC infections. The peptides also increase the antimicrobial activity of  
 CC neutrophils. The peptides overall effect cellular disruption and rapid  
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences  
 CC used in the exemplification of the present invention

XX SQ Sequence 16 AA;

Query Match 100.0% Score 83; DB 2; length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0;

OY 1 ADSGEGRPLAEGGGVR 16  
 Db 1 ADSGEGRPLAEGGGVR 16

RESULT 4

Query Match	100.0%	Score	83;	DB	2;	Length	16;			
Best Local Similarity	100.0%	Pred.	No.	1.3e-05;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	16;	Conservative	0;							

OY 1 ADSGEGRPLAEGGGVR 16  
 Db 1 ADSGEGRPLAEGGGVR 16

XX ID ABB56219 standard; peptide, 16 AA.

XX AC ABB56219;

XX SQ 1 ADSGEGRPLAEGGGVR 16

OY 1 ADSGEGRPLAEGGGVR 16

DT 15-FEB-2002 (first entry)  
 XX DE Vascular dementia-associated protein isoform (VPI) 419.  
 XX DE  
 KW Vasculair Dementia; VD; VD-associated protein isoform; VPI; screening;  
 KW diagnosis; prognosis; gene therapy.  
 XX OS Homo sapiens.  
 XX PN WO200169261-A2.  
 XX PD 20-SEP-2001.  
 XX PR 14-MAR-2001; 2001WO-GB001106.  
 XX PR 15-MAR-2000; 2000GB-00006285.  
 XX PR 24-NOV-2000; 2000GB-00028734.  
 XX PR 28-NOV-2000; 2000US-00724391.  
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX PI Herath HMA, Parekh RB, Rohlf C;  
 DR XX  
 PS WPI; 2001-557937/52.  
 XX  
 PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, for comprising analysing body fluid by 2-dimensional electrophoresis, for PT features correlated with VD.  
 XX  
 CC claim 6; Page 39, 151pp; English.  
 CC The invention relates to screening, diagnosis or prognosis of vascular dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of CC features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy  
 XX SQ sequence 16 AA:  
 Query Match 100.0%; Score 83; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ADSGEGDPLAEGGVR 16  
 Db 1 ADSGEGDPLAEGGVR 16  
 RESULT 5  
 AAB9159 ID AAB9159 standard; peptide; 16 AA.  
 AC AAB9159;  
 XX DT 22-JUN-2001 (first entry)  
 DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1135.  
 KW protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimido; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 OS Homo sapiens.

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OS Synthetic.  
 XX PN WO200069900-A2.  
 XX PD 23-NOV-2000.  
 XX PR 17-MAY-2000; 2000WO-US013576.  
 XX PR 17-MAY-1999; 99US-0134406P.  
 XX PR 10-SEP-1999; 99US-0153406P.  
 XX PR 15-OCT-1999; 99US-0159783P.  
 XX PA (CONJ-) CONUTCHEM INC.  
 XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 XX DR WPI; 2001-112059/12.  
 PS Modifying and attaching therapeutic peptides to albumin prevents PT peptidase degradation, useful for increasing length of in vivo activity.  
 XX Disclosure; Page 567; 733pp; English.  
 XX  
 CC The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidoyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptide stabilised therapeutic peptide composed of 3-50 amino acids (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention  
 XX SQ Sequence 16 AA:  
 Query Match 100.0%; Score 83; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ADSGEGDPLAEGGVR 16  
 Db 1 ADSGEGDPLAEGGVR 16  
 RESULT 6  
 ABB5237 ID ABB5237 standard; peptide; 16 AA.  
 AC ABB5237;  
 XX DT 08-FEB-2002 (first entry)  
 DE Human API-118 tryptic digest peptide #2.  
 KW Human; neuroprotective; nootropic; gene therapy; vaccine;  
 KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF; Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest; Expression Reference Protein Isoform; ERIF; proteolysis.  
 KW Expression Reference Protein Isoform; ERIF; proteolysis.  
 XX OS Homo sapiens.  
 XX PN WO200175454-A2.  
 XX PD 11-OCT-2001.

PF 03-APR-2001; 2001WO-US010908.  
 XX PT identifying compounds that modify interaction of gp120 and co-receptors,  
 PR 03-APR-2000; 2000US-0194504P.  
 PR PT also new peptides.  
 XX  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PA (Pfizer) PFIZER INC.  
 PA DR  
 PI Durham KU, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;  
 PI Pottier DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;  
 PI Townsend RR, White F, Williams SA;  
 XX WPI; 2001-639384/73.  
 PS Example; Page 33; 162pp; English.  
 XX  
 CC The invention relates to methods for the screening, diagnosis and  
 CC prognosis of Alzheimer's disease. The methods involve the detection of  
 CC Alzheimer's Disease-Associated Features (AxDs) and Alzheimer's Disease-  
 CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or  
 CC plasma. The abundance of the AxDs and APIs is then normalised to an  
 CC expression reference protein isoform (ERPI) in order to determine whether  
 CC a patient is suffering from, or has a predisposition to, Alzheimer's  
 CC disease. The relative abundance of the AxDs and APIs correlates with the  
 CC severity of Alzheimer's disease. The present sequence is a peptide  
 XX produced from an API by proteolysis  
 SQ sequence 16 AA;

Query Match	100.0%	Score 83;	DB 4;	Length 16;
Best Local Similarity	100.0%	Pred. No.	1.3e-05;	
Matches	16;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

OY 1 ADSGEGDPLAEKGGR 16  
 OY 1 ADSGEGDPLAEKGGR 16

Db

RESULT 7  
 ID ABG73668  
 ID ABG73668 standard; peptide; 16 AA.  
 XX  
 AC ABG73668;  
 XX  
 DT 11-MAR-2003 (first entry)  
 XX DB Linear HIV-1 gp120 V3-loop derived peptide ligand SEQ ID 11.  
 XX KW 9p120; interaction; co-receptor; CXCR4; CCR5; refractive index; V3 loop;  
 KW 7-helix transmembrane receptor; glycopeptide; virucide; anti-HIV;  
 KW HIV infection.  
 OS Human immunodeficiency virus 1.  
 OS Synthetic.  
 XX PN D51013042-A1.  
 XX PD 26-SEP-2002.  
 XX PF 09-MAR-2001; 2001DE-01013042.  
 XX PR 09-MAR-2001; 2001DE-01013042.  
 XX PA (NOCH-) NOCHT INST TROPENMEDIZIN BERNHARD.  
 XX PI Schreiber M, Seifert A, Meyer B;  
 XX DR WPI; 2002-752120/82.

Query Match

100.0%	Score 83;	DB 5;	Length 16;	
Best Local Similarity	100.0%	Pred. No.	1.3e-05;	
Matches	16;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

OY 1 ADSGEGDPLAEKGGR 16  
 OY 1 ADSGEGDPLAEKGGR 16

Do Sequence 16 AA;

RESULT 8  
 ID ABG78739  
 ID ABG78739 standard; peptide; 16 AA.  
 XX AC ABG78739;  
 XX DT 29-NOV-2002 (first entry)  
 XX DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #287.  
 KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF;  
 KW human; multiple sclerosis-associated protein isoform; MSPI;  
 KW antiinflammatory; neuroprotective.  
 XX OS Homo sapiens.  
 XX PN WO200239604-A2.  
 XX PD 01-AUG-2002.  
 XX PR 25-JAN-2002; 2002WO-GB000330.  
 XX PR 26-JAN-2001; 2001US-0264404P.  
 XX PR 20-NOV-2001; 2001US-0331647P.  
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX PI Herath HMAC, Parekh RB, Rohlf C;  
 XX DR WPI; 2002-599812/64.  
 XX  
 PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.  
 PT determining the stage or severity of MS, comprises detecting the presence  
 PT of MS-associated features or protein isoforms by 2-dimensional  
 PT electrophoresis.  
 RS Disclosure; Page 32; 128pp; English.  
 XX  
 CC This invention relates to a novel method for screening or diagnosing

CC multiple sclerosis (MS) in a subject to determine the stage or severity  
 CC of MS, to identify a subject at risk of developing MS or to monitor the  
 CC effect of a therapy administered. The method comprises analysing a sample  
 CC body fluid from the subject by two-dimensional electrophoresis and  
 CC detecting the presence of multiple sclerosis-associated features (MSFs),  
 CC and multiple sclerosis-associated protein isoforms (MSPIs). The MSFs of  
 CC the invention correspond to spots identified on a 2D gel these protein  
 CC may have antiinflammatory or neuroprotective activity. The methods of the  
 CC invention and the compositions are useful for clinical screening,  
 CC diagnosis and treatment of MS, for monitoring the effectiveness of MS  
 CC treatment, for selecting participants in clinical trials, for identifying  
 CC patients most likely to respond to a particular therapeutic treatment and  
 CC for screening and developing drugs for treatment of MS. Agents that  
 CC modulate the expression or activity of an MSPI are useful for treating  
 CC MS, for preventing or delaying the onset or development of MS, to prevent  
 CC or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic  
 CC acids comprising a sequence encoding an MSPI, MSPI-related polypeptide,  
 CC or their fragments are useful for promoting MSPI function by gene  
 CC therapy. The present sequence represents a human multiple sclerosis  
 CC associated feature tryptic digest peptide of the invention  
 XX SQ Sequence 16 AA;

Query Match 100%; Score 83; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSEGEGDPLAEGGVR 16  
 ID ABG70000  
 Db 1 ADSEGEGDPLAEGGVR 16

RESULT 9  
 ID ABG70000;  
 AC ABG70000;  
 XX DT 21-OCT-2002 (first entry)  
 XX DE Antimicrobial peptide CS-FBPa.  
 XX OS Unidentified.

KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;  
 KW bacterial infection; fungal infection; fungicide; disinfectant;  
 KW preservative; foods; cosmetic; multiple antibiotic resistance.

PN WO200255554-A2.

PD 18-JUL-2002.  
 XX PP 24-AUG-2001; 2001WO-US041877.

PR 25-AUG-2000; 2000US-00648816.

PA (HARB-) HARBOR-UCLA RBS & EDUCATION INST.

PT Yeaman MR, Shen AJ;

DR WPI; 2002-590659/63.

XX PT New antimicrobial peptide composition for the prevention and treatment of  
 CC infections caused by organisms, such as bacteria and fungi, exhibiting  
 PT multiple antibiotic resistance.

PS Disclosure; Page 18; 221pp; English.

CC possible structures are fully described in the specification. Also  
 CC included are (1) an antimicrobial peptide composition for direct activity  
 CC or for potentiating antimicrobial agents active against organisms such as  
 bacteria and fungi comprising a peptide of 13-74 containing an amino acid  
 CC core sequence selected from truncations of the peptides described above,  
 CC and remodels, extensions, combinations and fusions; and (2)  
 CC antimicrobial peptides for potentiating antimicrobial activity of  
 CC leukocytes against organisms such as bacteria and fungi. The  
 CC antimicrobial peptides are useful as individual antimicrobial agents,  
 CC specifically against bacteria and fungi, agents in combination with other  
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of  
 CC conventional antimicrobials, agents that enhance the antimicrobial  
 CC functions of leukocytes, as disinfectants or preservatives for use in  
 CC foods and cosmetics and as agents to improve efficiency of molecular  
 CC biology techniques. Antimicrobial peptides of prior art have generally  
 CC been considered to have undesirable toxicity, immunogenicity and short  
 CC half-lives due to biodegradation. The peptides of the present invention  
 CC are based upon natural antimicrobial peptides that have potent and broad  
 CC spectrum activity against pathogens exhibiting multiple antibiotic  
 CC resistance. They exhibit lower inherent mammalian cell toxicities and  
 CC overcome problems of toxicity, immunogenicity, and shortness of duration  
 CC of effectiveness due to biodegradation, retaining activity in plasma and  
 CC disclosure but specifically excluded from the scope of the invention  
 XX SQ Sequence 16 AA;

Query Match 100%; Score 83; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSEGEGDPLAEGGVR 16  
 ID ABG69911  
 Db 1 ADSEGEGDPLAEGGVR 16

RESULT 10  
 ID ABG69911  
 AC ABG69911;

XX DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #23.

XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;  
 KW bacterial infection; fungal infection; fungicide; disinfectant;  
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;

XX KW mutant; mutein.

OS Oryctolagus cuniculus.

OS Synthetic.

PR WO200255554-A2.

PD 18-JUL-2002.

PP 24-AUG-2001; 2001WO-US041877.

XX DR WPI; 2002-590659/63.

XX PT New antimicrobial peptide composition for the prevention and treatment of  
 CC infections caused by organisms, such as bacteria and fungi, exhibiting  
 PT multiple antibiotic resistance.

XX PS Disclosure; Page 135; 221pp; English.

XX  
 CC The invention relates to an antimicrobial peptide composition for use  
 CC against organisms such as bacteria and fungi comprising a peptide of 5-  
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from  
 PMP-1 and PMP-2, platelet microbicidal protein), and retromers', extensions,  
 truncations, extensions, combinations, fusions and their derivatives. The  
 possible structures are fully described in the specification. Also  
 included are (1) an antimicrobial peptide composition for direct activity  
 or for potentiating antimicrobial agents active against organisms such as  
 bacteria and fungi comprising a peptide of 13-74 containing an amino acid  
 core sequence selected from truncations of the peptides described above,  
 and retromers, extensions, combinations and fusions; and (2)  
 antimicrobial peptides for potentiating antimicrobial activity of  
 leukocytes against organisms such as bacteria and fungi. The peptides  
 antimicrobials are useful as individual antimicrobial agents,  
 specifically against bacteria and fungi, agents in combination with other  
 antimicrobials, agents that enhance, potentiate or restore efficacy of  
 conventional antimicrobials, agents that enhance the antimicrobial  
 functions of leukocytes, as disinfectants or preservatives for use in  
 food and cosmetics and as agents to improve efficiency of molecular  
 biology techniques. Antimicrobial peptides of prior art have generally  
 been considered to have undesirable toxicity, immunogenicity and short  
 half-lives due to biodegradation. The peptides of the present invention  
 are based upon natural antimicrobial peptides that have potent and broad  
 spectrum activity against pathogens exhibiting multiple antibiotic  
 resistance. They exhibit lower inherent mammalian cell toxicities and  
 overcome problems of toxicity, immunogenicity, and shortness of duration  
 of effectiveness due to biodegradation, retaining activity in plasma and  
 serum. The present sequence is a rabbit PMP based antimicrobial peptide  
 XX Sequence 16 AA;

Query Match 100.0%; Score 83; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ADSGEGDFLAEGGV 16  
 Db 1 ADSGEGDFLAEGGV 16

RESULT 11

ID ABP60019 ABP60019 standard; peptide; 16 AA.  
 XX  
 AC ABP60019;  
 XX  
 DT 24-FEB-2003 (first entry)  
 XX  
 DE Biopolymer disease specific marker.  
 XX  
 KW Biopolymer; disease specific marker; marker; myocardial infarction;  
 KW alpha fibrinogen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200208716-A2.  
 PD 07-NOV-2002.  
 XX  
 PF 25-APR-2002; 2002WO-CA000577.  
 XX  
 PR 30-APR-2001; 2001US-00845765.  
 PA (SYN+) SYN X PHARMA INC.  
 XX  
 PT Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;  
 XX  
 DR WPI; 2003-111905/10.

PT New biopolymer marker or its analyte, useful for determining the presence  
 or absence of at least one particular disease state, such as myocardial  
 infarction.

XX  
 CC Claim 1; Page 28; 28pp; English.  
 XX  
 CC The invention relates to a biopolymer disease specific marker. The  
 CC biopolymer marker is useful in indicating at least one particular disease  
 state, such as myocardial infarction. The method is useful for evidencing  
 CC and categorising at least one biopolymer marker sequence to determine the  
 presence or absence of at least one disease state. This marker is  
 CC characterised as an alpha fibrinogen having a molecular weight of 1518  
 CC daltons. The current sequence represents the biopolymer disease specific  
 CC marker of the invention

SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ADSGEGDFLAEGGV 16  
 Db 1 ADSGEGDFLAEGGV 16

RESULT 12

ID ABP60640 ABP60640 standard; peptide; 16 AA.  
 XX  
 AC ABP60640;  
 XX  
 DT 28-MAR-2003 (first entry)  
 XX  
 DE Fibrinopeptide A.  
 XX  
 KW Fibrinopeptide A; N-terminus; protein identification.  
 OS Unidentified.  
 XX  
 PN WO200295419-A2.  
 PD 28-NOV-2002.  
 XX  
 PF 20-MAY-2002; 2002WO-US016347.  
 XX  
 PR 23-MAY-2001; 2001US-00863786.  
 PR 20-DEC-2001; 2001US-0343019P.  
 XX  
 PA (AMSH ) AMERSHAM BIOSCIENCES AB.  
 PA (PROC ) PROCTER & GAMBLE CO.  
 XX  
 PI Bhikhahai R, Liminga M, Maloisel J, Palmgren R, Keough TW;  
 PI Youngquist RS, Vaughn HL, Yelm KE;  
 DR WPI; 2003-175111/17.

XX  
 PT Identification of polypeptide useful in proteomics, involves  
 PT derivatizing N-terminal or N-terminal of polypeptides with acidic reagent  
 PT containing sulfonyl or sulfonic acid moiety coupled to activated ester  
 XX  
 PS Example 3; Page 29; 90pp; English.

XX  
 CC The invention relates to a novel method for the identification of a  
 CC polypeptide involving a step of derivatising the N-terminal of the  
 CC polypeptide or the N-terminal of one or more polypeptides with acidic  
 CC reagent containing a sulfonyl or sulfonic acid moiety coupled to an  
 activated ester moiety, analysing the derivative using mass spectrometry  
 CC and interpreting the resulting fragmentation pattern. The present  
 sequence represents Fibrinopeptide A, used in example 3 of the invention  
 XX Sequence 16 AA;

Query Match 100.0%; Score 83; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 16; conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSEGEGDPLAEGGVR 16  
 ID ADA18542 standard; peptide; 16 AA.  
 Db 1 AUSGESEGDFLAEGGVR 16

RESULT 13  
 ADA18542  
 DT 20-NOV-2003 (first entry)  
 XX DE Human alpha fibrinogen peptide #2.  
 KW Alpha fibrinogen; human; myocardial infarction; SELDI; mass spectrometry;  
 KW surfaces enhanced for laser desorption/ionisation.

OS Homo sapiens.

XX PN US2002160423-A1.

PD 31-OCT-2002.

XX PF 30-APR-2001; 2001US-00846780.

PR 30-APR-2001; 2001US-00846780.

XX PA (JACK/ ) JACKOWSKI G.  
 PA (THAT/ ) THATCHER B.  
 PA (MARS/ ) MARSHALL J.  
 PA (YANT/ ) YANTRA J.  
 PA (VREE/ ) VREES T.

XX PI JACKOWSKI G., Thatcher B., Marshall J., Yantha J., Vrees T;  
 DR WPI; 2003-219987/21.

XX PT Biopolymer marker useful in indicating particular disease state  
 PT particularly myocardial infarction.

XX PS Claim 1; Page 7; 10pp; English.

XX CC The invention relates to a biopolymer marker useful in indicating at least one particular disease state. This marker is characterised as alpha fibrinogen having a molecular weight of 1536 Daltons and is useful for indicating a disease state, in particular myocardial infarction. The marker sequences are useful as antigens in immunoassays for the detection of those individuals suffering from the disease known to be evidenced by the marker sequence. The marker provides an efficient diagnostic tool for rapidly and accurately diagnosing disease states such as myocardial infarction. The marker was detected by the technique of surfaces enhanced for laser desorption/ionisation (SELDI) mass spectroscopy. The present sequence is the alpha fibrinogen marker peptide.

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSEGEGDPLAEGGVR 16  
 ID AUSGESEGDFLAEGGVR 16  
 Db 1 AUSGESEGDFLAEGGVR 16

RESULT 15  
 ADR51340  
 DT 12-FEB-2004 (first entry)  
 XX DE Antiangiogenic fibrinogen derived peptide 66.  
 KW fibrinogen; antiangiogenic; cytostatic; angiogenesis; gene therapy;  
 KW cancer; human; mutant; mutein.

XX OS Synthetic.  
 OS Homo sapiens.

XX FH Key-Modified-site 1 Location/Qualifiers  
 FT /note= "N-terminal acetyl"

RESULT 14  
 ABR58740  
 ID ABR58740 standard; peptide; 16 AA.  
 XX AC ABR58740;

FT Modified-site 16 /note= "C-terminal amide"  
 FT XX  
 PN WO2003070769-A2.  
 XX  
 PD 28-AUG-2003.  
 XX  
 PF 19-FEB-2003; 2003WO-EP001698.  
 XX  
 PR 19-FEB-2002; 2002GB-00003882.  
 PR 19-FEB-2002; 2002GB-00003883.  
 PR 23-JUL-2002; 2002GB-00017067.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS PHARMA GMBH.  
 PA (BIOA-) BIOACTA LTD.  
 XX  
 PI Garcia-Echeverria C, Lewis C, Robinson J,  
 XX DR WPI; 2003-731548/69.  
 XX PT New polypeptide derived from fibrinogen and having anti-angiogenic  
 PT activity, useful for preparing a composition for treating cancer.  
 XX  
 PS Example 37; Fig 3; 66pp; English.  
 XX  
 CC This invention relates to a novel polypeptide derived from fibrinogen  
 CC comprising 15 or less amino acids which has antiangiogenic activity. The  
 CC invention may be useful for the development of compounds with a  
 CC cytostatic activity through the inhibition of angiogenesis. The sequences  
 CC of the invention may be useful for gene therapy. The polypeptide is  
 CC useful for inhibiting angiogenesis and in preparing a composition for  
 CC treating cancer.  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 83; DB 7; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ADSGEGDFIAEGGVR	16
Db	1	ADSGEGDFIAEGGVR	16

Search completed: January 21, 2005, 08:31:10  
 Job time : 88 secs

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GenCore version 5.1.16

OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:52 : Search time 26 Seconds  
(without alignments)  
40.811 Million cell updates/sec

Title: US-09-845-765-1  
Perfect score: 83  
Sequence: 1 ASGEGGPPLAKGGVVR 16

Scoring table: BLOSUM62  
Gappen 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
 1: /cggn2\_6/podata/1/iaa/5A-COMB pep: \*  
 2: /cggn2\_6/podata/1/iaa/5B-COMB pep: \*  
 3: /cggn2\_6/podata/1/iaa/6A-COMB pep: \*  
 4: /cggn2\_6/podata/1/iaa/6B-COMB pep: \*  
 5: /cggn2\_6/podata/1/iaa/CTUS-COMB.pep: \*  
 6: /cggn2\_6/podata/1/iaa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	16	2	US-08-796-598-14 Sequence 14, Appl Sequence 14, Appl
2	83	100.0	16	2	US-08-796-598-14 Sequence 14, Appl Sequence 14, Appl
3	83	100.0	16	3	US-08-796-141A-55 Sequence 55, Appl Sequence 55, Appl
4	83	100.0	16	4	US-09-525-289A-25 PCT-US5-1794-55 Sequence 55, Appl Sequence 55, Appl
5	83	100.0	16	5	US-09-525-289A-25 PCT-US5-1794-55 Sequence 55, Appl Sequence 55, Appl
6	83	100.0	17	4	US-09-545-719B-1 US-08-796-141A-55 Sequence 55, Appl Sequence 55, Appl
7	83	100.0	18	3	US-08-796-141A-55 PCT-US5-1794-55 Sequence 55, Appl Sequence 55, Appl
8	83	100.0	18	5	US-08-796-141A-54 PCT-US5-1794-54 Sequence 54, Appl Sequence 54, Appl
9	83	100.0	19	3	US-08-796-141A-54 PCT-US5-1794-54 Sequence 54, Appl Sequence 54, Appl
10	83	100.0	19	5	US-08-796-657-1 US-07-984-884-1 US-08-881-810-1 US-08-884-426-1 US-08-880-818-1 Sequence 54, Appl Sequence 54, Appl
11	83	100.0	20	1	US-09-225-269A-52 PCT-US5-13794-52 Sequence 52, Appl Sequence 52, Appl
12	83	100.0	20	1	US-09-225-269A-52 PCT-US5-13794-52 Sequence 52, Appl Sequence 52, Appl
13	83	100.0	20	1	US-08-881-810-1 US-08-884-426-1 US-08-880-818-1 Sequence 54, Appl Sequence 54, Appl
14	83	100.0	20	2	US-08-880-818-1 US-08-884-426-1 US-08-880-818-1 Sequence 54, Appl Sequence 54, Appl
15	83	100.0	20	3	US-08-888-657-1 US-07-984-884-1 US-08-881-810-1 US-08-884-426-1 US-08-880-818-1 Sequence 53, Appl Sequence 53, Appl
16	83	100.0	20	3	US-09-225-269A-53 PCT-US5-13794-53 US-08-869-141A-45 PCT-US5-13794-45 US-08-869-141A-44 US-08-869-141A-44 Sequence 53, Appl Sequence 53, Appl
17	83	100.0	20	5	US-09-225-269A-52 PCT-US5-13794-52 US-08-869-141A-45 PCT-US5-13794-45 US-08-869-141A-44 US-08-869-141A-44 Sequence 52, Appl Sequence 52, Appl
18	83	100.0	20	5	US-09-225-269A-52 PCT-US5-13794-52 US-08-869-141A-45 PCT-US5-13794-45 US-08-869-141A-44 US-08-869-141A-44 Sequence 52, Appl Sequence 52, Appl
19	83	100.0	21	3	US-08-869-141A-45 PCT-US5-13794-45 US-08-869-141A-44 US-08-869-141A-44 Sequence 53, Appl Sequence 53, Appl
20	83	100.0	21	5	US-08-869-141A-45 PCT-US5-13794-45 US-08-869-141A-44 US-08-869-141A-44 Sequence 54, Appl Sequence 54, Appl
21	83	100.0	22	3	US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 Sequence 52, Appl Sequence 52, Appl
22	83	100.0	22	5	US-08-869-141A-44 PCT-US5-13794-44 PCT-US5-13794-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 Sequence 52, Appl Sequence 52, Appl
23	83	100.0	22	5	US-08-869-141A-44 PCT-US5-13794-44 PCT-US5-13794-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 Sequence 52, Appl Sequence 52, Appl
24	83	100.0	22	5	US-08-869-141A-44 PCT-US5-13794-44 PCT-US5-13794-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 Sequence 52, Appl Sequence 52, Appl
25	83	100.0	23	3	US-08-869-141A-44 PCT-US5-13794-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 Sequence 52, Appl Sequence 52, Appl
26	83	100.0	25	3	US-08-869-141A-44 PCT-US5-13794-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 Sequence 52, Appl Sequence 52, Appl
27	83	100.0	25	3	US-08-869-141A-44 PCT-US5-13794-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 US-08-869-141A-44 Sequence 52, Appl Sequence 52, Appl

**ALIGNMENTS**

RESULT 1  
US-08-796-598-14  
; Sequence 14, Application US/08796598  
; Patent No. 5927659

GENERAL INFORMATION:

APPLICANT: TARR, GEORGE E.  
TITLE OF INVENTION: METHODS AND APPARATUS FOR POLYMERS USING MASS SPECTRUM NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADRESSEE: Patent Administrator - Testa, Hu ADDRESSE: Thibault STREET: High Street Tower, 125 High Street CITY: Boston STATE: MA COUNTRY: USA ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, version #11 CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/796,598 FILING DATE: 07-FEB-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,055 FILING DATE: 19-MAY-1995 ATTORNEY/AGENT INFORMATION:  
NAME: FLYNN ESG., Kerry A. REGISTRATION NUMBER: 33,693 REFERENCE/DOCKET NUMBER: SYP-115 TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000 TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

Query Match Best Local Similarity 100.0%; Score 83; DB 2; Matches 16; Conservative 0; Mismatches 0; Gapopen 0; Gapext 0; Sequence 16, Appl Sequence 16, Appl

**RESULT 1**

US-08-796-598-14 Application US/08796598  
 Sequence 14 Application US/08796598  
 Patent No. 5427659

GENERAL INFORMATION:

APPLICANT: PATTERSON, DALE H.  
 APPLICANT: TARR, GEORGE E.

TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING  
 TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patient Administrator - Teata, Hurwitz & Thibeault  
 STREET: High Street Tower, 125 High Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/796,598  
 FILING DATE: 07-FEB-1997  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,055  
 FILING DATE: 19-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: FLYNN Esq., Kerry A.  
 REGISTRATION NUMBER: 33,693  
 REFERENCE/DOCKET NUMBER: SIP-115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 24-7000  
 TELEFAX: (617) 248-7100  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 amino acid  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-08-796-598-14

Query Match 100 %; Score 83; DB 2; Length 16;  
 Best Local Similarity 100 %; Pred. No. 3.8e-06;  
 Mismatches 0; Indels 0; Gaps 0;

28 63 100.0 350 2 US-07-2051-350 Sequence, Appl  
 29 83 100.0 643 2 PCT-US93-12687-4 Sequence 4, Appl  
 30 83 100.0 643 5 PCT-US95-33794-46 Sequence 4, Appl  
 31 83 100.0 644 1 US-08-206-176-2 Sequence 2, Appl  
 32 83 100.0 644 1 US-09-1919-039-121 Sequence 121, App  
 33 83 100.0 847 4 US-09-373-157-4 Sequence 4, Appl  
 34 69 83.1 14 4 US-09-845-725A-1 Sequence 1, Appl  
 35 63 75.9 17 5 US-08-692-141A-6 Sequence 46, Appl  
 36 63 75.9 17 5 PCT-US95-33794-46 Sequence 46, Appl  
 37 58 69.9 12 4 US-09-846-350A-1 Sequence 1, Appl  
 38 58 69.9 28 6 5196404-16 Sequence 1, Appl  
 39 53 63.9 10 6 5196404-18 Sequence 1, Appl  
 40 53 63.9 10 6 5433940-25 Sequence 1, Appl  
 41 52 62.7 15 3 US-08-469-141A-6 Sequence 6, Appl  
 42 52 62.7 15 5 PCT-US95-13794-6 Sequence 6, Appl  
 43 52 62.7 24 2 US-08-978-004B-48 Sequence 48, Appl  
 44 46 55.4 17 11 US-08-92-553-11 Sequence 11, Appl  
 45 46 55.4 17 4 US-09-129-192C-45 Sequence 45, Appl  

ALIGNMENTS

QY 1 ADSGEGDFLAEGGGVR 16  
1 ADSGEGDFLAEGGGVR 16

RESULT 2  
US-08-447-175A-14 Application US/08447175A  
Sequence 14; Application US/08447175A  
Patent No. 586940  
GENERAL INFORMATION:  
APPLICANT: PATTERSON, DALE H.  
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING POLYMERS WITH A STATISTICAL CERTAINTY USING MASS SPECTROMETRY.  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patent Administrator - Testa, Hurwitz & Stern, LLP  
STREET: High Street Tower, 125 High Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/447,175A  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 422  
ATTORNEY/AGENT INFORMATION:  
NAME: RAUSCHENBACH, Kurt  
REGISTRATION NUMBER: 40,137  
REFERENCE/DOCKET NUMBER: SIP-114  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-447-175A-14

Query Match 100.0%; Score 83; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSGEGDFLAEGGGVR 16  
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 3  
US-08-461-141A-56  
; sequence 56, Application US/0846141A  
; Patent No. 612410/  
; GENERAL INFORMATION:  
; APPLICANT: MOMFORD, RICHARD A.  
; APPLICANT: DAVIES, D.T. PHILIP  
; APPLICANT: DAHLGREN, MARY E.  
; APPLICANT: BOGER, JOSHUA S.  
; APPLICANT: HOMES, JOHN L.  
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN POLYMERONUCLEAR LEUKOCYTE ELASTASE ACTIVITY  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DR. CHRISTINE E. CARTY  
; STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000

Query Match 100.0%; Score 83; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSGEGDFLAEGGGVR 16

Query Match 100.0%; Score 83; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSGEGDFLAEGGGVR 16  
Db 1 ADSGEGDFLAEGGGVR 16

RESULT 4  
US-09-525-269A-25  
Query Match 100.0%; Score 83; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSGEGDFLAEGGGVR 16  
Db 1 ADSGEGDFLAEGGGVR 16

Query Match 100.0%; Score 83; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSGEGDFLAEGGGVR 16  
Db 1 ADSGEGDFLAEGGGVR 16

Query Match 100.0%; Score 83; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSGEGDFLAEGGGVR 16  
Db 1 ADSGEGDFLAEGGGVR 16

Query Match 100.0%; Score 83; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSGEGDFLAEGGGVR 16  
Db 1 ADSGEGDFLAEGGGVR 16

Db 1 ADSGGDFLAGGGVR 16

RESULT 5

PCT-US95-13794-56

GENERAL INFORMATION:

; Sequence 56, Application PC/TUS9513794

; APPLICANT: Mumford, Richard A.

; APPLICANT: Davies, D.T. Philip

; APPLICANT: Dahlgren, Mary E.

; APPLICANT: Boger, Joshua S.

; APPLICANT: Humes, John L.

TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY

TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dr. Christine E. Carty

; STREET: 126 E. Lincoln Avenue, P.O. Box 2000

; CITY: Rahway

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07065-0907

COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/13794

; FILING DATE: 03-NOV-1995

CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Carty, Christine E.

; REGISTRATION NUMBER: 36,099

; REFERENCE/DOCKET NUMBER: 17461IAY

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 594-6734

; TELEFAX: (908) 594-6720

; INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

PCT-US95-13794-56

RESULT 6

; Sequence 1, Application US/09845719B

; Patient No. 662706

; GENERAL INFORMATION:

; APPLICANT: JACKOWSKI, George

; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR

; TITLE OF INVENTION: OF 1465 DALTONS

; FILE REFERENCE: 2132.035

; CURRENT APPLICATION NUMBER: US/09/845,719B

; CURRENT FILING DATE: 2001-04-30

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens

; US-09-845-719B-1

Query Match Best Local Similarity 100.0%; Score 83; DB 3; Length 17;

; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 1 ADSGGGDFLAGGGVR 16

; Db 1 ADSGGDFLAGGGVR 16

; RESULT 7  
; US-08-469-141A-55  
; Sequence 55, Application US/08469141A  
; Patent No. 6124107

; GENERAL INFORMATION:

; APPLICANT: MUMFORD, RICHARD A.

; APPLICANT: DAVIES, D.T. PHILIP

; APPLICANT: DAHLGREN, MARY E.

; APPLICANT: BOGER, JOSHUA S.

; APPLICANT: HUMES, JOHN L.

TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY

TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:

; ADDRESSEE: DR. CHRISTINE E. CARTY

; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000

; CITY: RAHWAY

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07065-0907

COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/469,141A

; FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: CARTY, CHRISTINE E.

; REGISTRATION NUMBER: 36,099

; REFERENCE/DOCKET NUMBER: 17461IB

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908)-594-6734

; TELEFAX: (908) 594-6720

; INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

US-08-469-141A-55

; Query Match Best Local Similarity 100.0%; Score 83; DB 3; Length 18;

; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 1 ADSGGGDFLAGGGVR 16

; Db 1 ADSGGDFLAGGGVR 16

; RESULT 8  
; PCT-US95-13794-55

Sequence 55, Application PC/US9513794  
GENERAL INFORMATION:  
APPLICANT: Mumford, Richard A.  
APPLICANT: Davies, D.T. Philip  
APPLICANT: Dahlgren, Mary E.  
APPLICANT: Boger, Joshua S.  
APPLICANT: Humes, John L.  
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Christine E. Carty  
STREET: 126 E. Lincoln Avenue; P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,141A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARTY, CHRISTINE E.  
REGISTRATION NUMBER: 36,099  
REFERENCE/DOCKET NUMBER: 174611B  
TELEPHONE: (908)-594-4720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)-594-6734  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDBEDNESS: single  
TOPOLogy: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-469-141A-54  
Query Match Score 83; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
PCR-US95-13794-55  
RESULT 9  
PCT-US95-13794-54  
Sequence 54, Application PC/US9513794  
GENERAL INFORMATION:  
APPLICANT: Mumford, Richard A.  
APPLICANT: Davies, D.T. Philip  
APPLICANT: Dahlgren, Mary E.  
APPLICANT: Boger, Joshua S.  
APPLICANT: Humes, John L.  
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Christine E. Carty  
STREET: 126 E. Lincoln Avenue; P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13794  
FILING DATE: 03-NOV-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Carty, Christine E.  
REGISTRATION NUMBER: 36,099  
REFERENCE/DOCKET NUMBER: 174611B  
TELEPHONE: (908) 594-4720  
TELEFAX: (908) 594-6734  
RESULT 10  
PCT-US95-13794-54  
Sequence 54, Application PC/US9513794  
GENERAL INFORMATION:  
APPLICANT: Mumford, Richard A.  
APPLICANT: Davies, D.T. Philip  
APPLICANT: Dahlgren, Mary E.  
APPLICANT: Boger, Joshua S.  
APPLICANT: Humes, John L.  
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Christine E. Carty  
STREET: 126 E. Lincoln Avenue; P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13794  
FILING DATE: 03-NOV-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Carty, Christine E.  
REGISTRATION NUMBER: 36,099  
REFERENCE/DOCKET NUMBER: 174611B  
TELEPHONE: (908) 594-4720  
TELEFAX: (908) 594-6734

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: internal

PCR-US95-13794-54

Query Match 100.0%; Score 83; DB 5; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGSR 16  
Db 1 ADSGEGDFLAEGGSR 16

RESULT 11  
US-08-288-657-1

Patent No. 5424291

GENERAL INFORMATION:

SEQUENCE 1, Application US/08288657

APPLICANT: Atrash, Butrus

APPLICANT: Jones, David M.

APPLICANT: Szelke, Michael

TITLE OF INVENTION: New Isoteric Peptides

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Richard J. Stern, Ph.D.

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/288,657

FILING DATE: 08/28/1991

ATTORNEY/AGENT INFORMATION:

NAME: Stern, Richard J.

REGISTRATION NUMBER: 35, 372

REFERENCE/DOCKET NUMBER: 1103326-016

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)819-8200

TELEFAX: (212)354-8113

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..20

OTHER INFORMATION: /note= "Peptide sequence containing

OTHER INFORMATION: thrombin cleavage site in the human fibrinogen

OTHER INFORMATION: *A-alpha chain.*"

FEATURE: Cleavage-site

NAME/KEY: Cleavage-site

LOCATION: 16..17

US-08-288-657-1

Query Match 100.0%; Score 83; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGSR 16  
Db 1 ADSGEGDFLAEGGSR 16

RESULT 12  
US-07-984-884-1

Sequence 1, Application US/07984884

PATENT NO. 5614499

GENERAL INFORMATION:

APPLICANT: Teger-Nilsson, Ann-Catrine E

APPLICANT: Bylund, Ruth E

TITLE OF INVENTION: New peptide derivatives

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: White and Case

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/984,884

FILING DATE: 02-DEC-1992

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stern, Richard J.

REGISTRATION NUMBER: 35, 372

REFERENCE/DOCKET NUMBER: 1103326-016

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)819-8200

TELEFAX: (212)354-8113

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

RESULT 13  
US-08-481-810-1

Sequence 1, Application US/08481810

PATENT NO. 5736221

GENERAL INFORMATION:

APPLICANT: Teger-Nilsson, Ann-Catrine E

APPLICANT: Bylund, Ruth E  
 TITLE OF INVENTION: New peptide derivatives  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: White and Case  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States  
 ZIP: 10036-2787  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/481,810  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/984884  
 FILING DATE: 02-DEC-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stern, Richard J  
 REGISTRATION NUMBER: 35,372  
 REFERENCE/DOCKET NUMBER: 1103326-016  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 819-8200  
 TELEFAX: (212) 354-8113  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 REFERENCE/DOCKET NUMBER: 1103326-016  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 819-8200  
 TELEFAX: (212) 354-8113  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 MOLECULE TYPE: peptide  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-481-810-1

Query Match 100.0%; Score 83; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADSGEGDFLAEGGAVR 16  
 Db 1 ADSGEGDFLAEGGAVR 16

RESULT 14  
 US-08-484-426-1  
 ; Sequence 1, Application US/08484426  
 ; Patent No. 574760  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Teger-Nilsson, Ann-Catrine E  
 ; TITLE OF INVENTION: New peptide derivatives  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: White and Case  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: United States  
 ; ZIP: 10036-2787  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,818  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/984884  
 FILING DATE: 02-DEC-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stern, Richard J  
 REGISTRATION NUMBER: 35,372  
 REFERENCE/DOCKET NUMBER: 1103326-016  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 819-8200  
 TELEFAX: (212) 354-8113  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 MOLECULE TYPE: peptide  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-484-426-1

Query Match 100.0%; Score 83; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADSGEGDFLAEGGAVR 16  
 Db 1 ADSGEGDFLAEGGAVR 16

RESULT 15  
 US-08-480-818-1  
 ; Sequence 1, Application US/08480818  
 ; Patent No. 5955433  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Teger-Nilsson, Ann-Catrine E  
 ; TITLE OF INVENTION: New peptide derivatives  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: White and Case  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: United States  
 ; ZIP: 10036-2787  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,818  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/984884  
 FILING DATE: 02-DEC-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stern, Richard J  
 REGISTRATION NUMBER: 35,372  
 REFERENCE/DOCKET NUMBER: 1103326-016  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 819-8200  
 TELEFAX: (212) 354-8113  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 MOLECULE TYPE: peptide  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-480-818-1

; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
US-08-480-818-1

Query Match 100.0%; Score 83; DB 2; Length 20;  
Best local Similarity 100.0%; Pred. No. 4.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0;  
Oy 1 ADSEGEGDFLAEGGGVR 16  
Db 1 ADSEGEGDFLAEGGGVR 16

Search completed: January 21, 2005, 08:29:37  
Job time : 28 secs

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### OM protein - protein search, using SW model

Run on: January 21, 2005, 08:04:53 ; Search time 75 Seconds

(without alignments)  
77.075 Million cell updates/sec

Title: US-09-845-765-1  
Perfect score: 83  
Sequence: 1 ADSGEGDFLAEGGGVR 16

Scoring table: BLOSUM62  
Gapext 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters:

1608061

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/pctodata/2/pubpaa/us07\_pubcomb.pep: \*  
2: /cgn2\_6/pctodata/2/pubpaa/pct-new\_pub.pep: \*  
3: /cgn2\_6/pctodata/2/pubpaa/us06\_pubcomb.pep: \*  
4: /cgn2\_6/pctodata/2/pubpaa/us06\_pubcomb.pep: \*  
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6: /cgn2\_6/pctodata/2/pubpaa/pctus\_pubcomb.pep: \*  
7: /cgn2\_6/pctodata/2/pubpaa/us08\_pubcomb.pep: \*  
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10: /cgn2\_6/pctodata/2/pubpaa/us09\_pubcomb.pep: \*  
11: /cgn2\_6/pctodata/2/pubpaa/us09c\_pubcomb.pep: \*  
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13: /cgn2\_6/pctodata/2/pubpaa/us10\_pubcomb.pep: \*  
14: /cgn2\_6/pctodata/2/pubpaa/us10\_pubcomb.pep: \*  
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16: /cgn2\_6/pctodata/2/pubpaa/us10\_pubcomb.pep: \*  
17: /cgn2\_6/pctodata/2/pubpaa/us10\_new\_pub.pep: \*  
18: /cgn2\_6/pctodata/2/pubpaa/us11\_new\_pub.pep: \*  
19: /cgn2\_6/pctodata/2/pubpaa/usgo\_new\_pub.pep: \*  
20: /cgn2\_6/pctodata/2/pubpaa/us60\_pubcomb.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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US-09-845-780-1

RESULT 1  
US-09-845-780-1  
; Sequence 1, Application US/09846780  
; Patent No. US20020160423A1

#### GENERAL INFORMATION:

APPLICANT: Jackowski, George

TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR

TITLE OF INVENTION: OF 1563 DALTONS

FILE REFERENCE: 2132\_039

CURRENT APPLICATION NUMBER: US/09/846,780

CURRENT FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 1

LENGTH: 16

TYPE: PRT

ORGANISM: Homo sapiens

US-09-845-780-1

RESULT 2  
US-09-826-290-352

; Sequence 352, Application US/09826290

; Patent No. US200164668A1

; GENERAL INFORMATION:

; APPLICANT: Durham, L.Kathryn

; APPLICANT: Friedman, David L.

; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri

Query Match Score: 100.0%; DB 9; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSGEGDFLAEGGGVR 16

Dy 1 ADSGEGDFLAEGGGVR 16

#	Query Match	Score	DB	Length	Indels	Gaps	Organism
1	US-09-845-780-1	83	100.0	24	17	US-10-845-568-3	Sequence 3, Appli
15	83	100.0	24	17	US-10-845-568-10	Sequence 10, Appli	
16	83	100.0	24	17	US-10-845-568-25	Sequence 15, Appli	
17	83	100.0	24	17	US-10-845-568-40	Sequence 40, Appli	
18	83	100.0	24	17	US-10-845-568-41	Sequence 41, Appli	
19	83	100.0	24	17	US-10-845-568-42	Sequence 42, Appli	
20	83	100.0	24	17	US-10-845-568-43	Sequence 43, Appli	
21	83	100.0	24	17	US-10-845-568-44	Sequence 44, Appli	
22	83	100.0	24	17	US-10-845-568-45	Sequence 45, Appli	
23	83	100.0	24	17	US-10-845-568-46	Sequence 46, Appli	
24	83	100.0	24	17	US-10-845-568-47	Sequence 47, Appli	
25	83	100.0	24	17	US-10-845-568-48	Sequence 48, Appli	
26	83	100.0	24	17	US-10-845-568-49	Sequence 49, Appli	
27	83	100.0	25	9	US-09-757-774-16	Sequence 16, Appli	
28	83	100.0	28	17	US-10-845-568-61	Sequence 17, Appli	
29	83	100.0	28	17	US-10-845-568-62	Sequence 18, Appli	
30	83	100.0	78	15	US-10-363-369-15	Sequence 19, Appli	
31	83	100.0	360	9	US-09-922-297-587	Sequence 20, Appli	
32	83	100.0	388	15	US-10-236-392-34	Sequence 21, Appli	
33	83	100.0	481	15	US-10-236-392-36	Sequence 22, Appli	
34	83	100.0	620	10	US-09-931-0094-1	Sequence 23, Appli	
35	83	100.0	644	10	US-09-919-039-121	Sequence 24, Appli	
36	83	100.0	644	15	US-10-236-392-32	Sequence 25, Appli	
37	83	100.0	847	13	US-10-112-527-4	Sequence 26, Appli	
38	80	96.4	15	14	US-10-359-363-25	Sequence 27, Appli	
39	80	96.4	24	17	US-10-484-568-27	Sequence 28, Appli	
40	79	95.2	15	9	US-09-845-568-1	Sequence 29, Appli	
41	79	95.2	15	17	US-10-484-568-51	Sequence 30, Appli	
42	79	95.2	23	17	US-10-484-568-63	Sequence 31, Appli	
43	79	95.2	24	17	US-10-484-568-63	Sequence 32, Appli	
44	78	94.0	15	17	US-10-484-568-50	Sequence 33, Appli	
45	78	94.0	15	17	US-10-363-369-7	Sequence 34, Appli	

### ALIGNMENTS

QY	Dy	Score	DB	Length	Indels	Gaps	Organism
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-3	Sequence 3, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-10	Sequence 10, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-25	Sequence 15, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-40	Sequence 40, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-41	Sequence 41, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-42	Sequence 42, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-43	Sequence 43, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-44	Sequence 44, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-45	Sequence 45, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-46	Sequence 46, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-47	Sequence 47, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-48	Sequence 48, Appli
1 ADSGEGDFLAEGGGVR 16	1 ADSGEGDFLAEGGGVR 16	83	100.0	24	17	US-10-845-568-49	Sequence 49, Appli

FILE REFERENCE: 22118.0001U4  
 CURRENT APPLICATION NUMBER: US/10/359,363A  
 CURRENT FILING DATE: 2003-02-05  
 PRIOR APPLICATION NUMBER: 601429,278  
 PRIOR FILING DATE: 2002-11-25  
 PRIOR APPLICATION NUMBER: 601392,133  
 PRIOR FILING DATE: 2002-06-28  
 PRIOR APPLICATION NUMBER: 601354,678  
 PRIOR FILING DATE: 2002-02-06  
 NUMBER OF SEQ ID NOS: 104  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 2  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1  
 OTHER INFORMATION: Synthetic Construct  
 US-10-359-363A-2  

Query Match      Score 83; DB 9; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSGEGDFLAEGGVR 16  
 Db      1 ADSGEGDFLAEGGVR 16

RESULT 3  
 US-09-845-765-1  
 Sequence 1, Application US/09845765  
 Publication No. US20040198950A1  
 GENERAL INFORMATION:

APPLICANT: JACKOWSKI, George  
 TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR  
 FILE REFERENCE: 2132.036  
 CURRENT APPLICATION NUMBER: US/09/845,765  
 CURRENT FILING DATE: 2001-04-30  
 NUMBER OF SEQ ID NOS: 1  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-845-765-1

Query Match      Score 83; DB 12; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSGEGDFLAEGGVR 16  
 Db      1 ADSGEGDFLAEGGVR 16

RESULT 5  
 US-10-264-309-8  
 Sequence 8, Application US/10264309  
 Publication No. US20040022794A1  
 GENERAL INFORMATION:

APPLICANT: FRIEDMAN, DAVID L.  
 APPLICANT: HERATH, HERATH  
 APPLICANT: KIMMEL, LIDA H.  
 APPLICANT: PAREKH, RAJESH B.  
 APPLICANT: POTTER, DAVID M.  
 APPLICANT: ROHLFF, CHRISTIAN  
 APPLICANT: SIBER, B. MICHAEL  
 APPLICANT: SNIDER, PETER J.  
 APPLICANT: SOARES, HOLLY D.  
 APPLICANT: STIGER, THOMAS R.  
 APPLICANT: SUNDERLAND, P. TREY  
 APPLICANT: TOWNSEND, ROBERT R.  
 APPLICANT: WHITE, W. FROST  
 APPLICANT: WILLIAMS, STEPHEN A.  
 TITLE OF INVENTION: NUCLEAR ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR  
 TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE  
 FILE REFERENCE: POA-002.01  
 CURRENT APPLICATION NUMBER: US/10/264,309  
 CURRENT FILING DATE: 2002-10-03  
 PRIOR APPLICATION NUMBER: 601326,708  
 NUMBER OF SEQ ID NOS: 491  
 SOFTWARE: PatentIn Version 2.1  
 SEQ ID NO: 8  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-264-309-8

Query Match      Score 83; DB 15; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSGEGDFLAEGGVR 16  
 Db      1 ADSGEGDFLAEGGVR 16

RESULT 4  
 US-10-359-363A-2  
 Sequence 2, Application US/10359363A  
 Publication No. US20030228371A1  
 GENERAL INFORMATION:  
 APPLICANT: SKINNER, James E.  
 APPLICANT: Anchim, Jerry M.  
 TITLE OF INVENTION: ANTI-INFARCTION MOLECULES

RESULT 6  
US-10-325-162-1  
; Sequence 1, Application US/10325162  
; Publication No. US20040121306A1  
; GENERAL INFORMATION:  
; APPLICANT: Marshall, John  
; APPLICANT: Jackowski, George  
; TITLE OF INVENTION: Method of Confirming the Presence of Myocardial Infarction  
; FILE REFERENCE: 2132.132  
; CURRENT APPLICATION NUMBER: US/10/325,162  
; CURRENT FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-325-162-1

Query Match 100.0%; Score 83; DB 16; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSEGDFLAEGGYR 16  
Db 1 ADSEGDFLAEGGYR 16

RESULT 7  
US-10-484-568-6  
; Sequence 60, Application US/10484568  
; Publication No. US2004024194A1  
; GENERAL INFORMATION:  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Lewis, Claire  
; APPLICANT: Robinson, Jeffrey  
; TITLE OF INVENTION: Peptide Screen  
; FILE REFERENCE: 4-32520A/32360/361  
; CURRENT APPLICATION NUMBER: US/10/484,568  
; CURRENT FILING DATE: 2004-01-22  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 60  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-484-568-60

Query Match 100.0%; Score 83; DB 17; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGRGDFLAEGGVR 16  
Db 1 ADSGRGDFLAEGGVR 16

RESULT 8  
US-10-197-954-53  
; Sequence 53, Application US/10197954  
; Publication No. US2003011902A1  
; GENERAL INFORMATION:  
; APPLICANT: K"ster, Hubert  
; APPLICANT: Stodiqi, Suhail  
; APPLICANT: Little, Daniel  
; TITLE OF INVENTION: Capture Compounds, Collections Thereof And Methods For Analyzing The Proteome And Complex  
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex  
; FILE REFERENCE: 2473-2305  
; CURRENT APPLICATION NUMBER: US/10/197,954  
; CURRENT FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: 60/306,019

Query Match 100.0%; Score 83; DB 17; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSGRGDFLAEGGVR 16  
Db 1 ADSGRGDFLAEGGVR 16

RESULT 9  
US-10-363-369-3  
; Sequence 3, Application US/10363369  
; Publication No. US20040039157A1  
; GENERAL INFORMATION:  
; APPLICANT: Biocata Limited  
; TITLE OF INVENTION: Anti-Angiogenic Peptides  
; FILE REFERENCE: P38123WO  
; CURRENT APPLICATION NUMBER: US/10/363,369  
; CURRENT FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: 0031475.9  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-363-369-3

Query Match 100.0%; Score 83; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSEGDFLAEGGYR 16  
Db 2 ADSEGDFLAEGGYR 17

RESULT 10  
US-10-363-369-4  
; Sequence 4, Application US/10363369  
; Publication No. US20040039157A1  
; GENERAL INFORMATION:  
; APPLICANT: Biocata Limited  
; TITLE OF INVENTION: Anti-Angiogenic Peptides  
; FILE REFERENCE: P38123WO  
; CURRENT APPLICATION NUMBER: US/10/363,369  
; CURRENT FILING DATE: 2003-06-23  
; PRIOR APPLICATION NUMBER: 0031475.9  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (23)..(23)  
; OTHER INFORMATION: any amino acid residue

US-10-363-369-4

Db ||||||| 1 ADSEGDFLAEGGVR 16

Query Match 100.0%; Score 83; DB 15; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSEGDFLAEGGVR 16  
 Db 1 ADSEGDFLAEGGVR 16

RESULT 11

US-10-363-365-5

Sequence 5, Application US/10333369

Publication No. US20040039157A1

GENERAL INFORMATION:

APPLICANT: Biocata Limited

TITLE OF INVENTION: Anti-Angiogenic Peptides

FILE REFERENCE: P38123WO

CURRENT APPLICATION NUMBER: US/10/363,369

CURRENT FILING DATE: 2003-06-23

PRIOR APPLICATION NUMBER: 0021475.9

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5

LENGTH: 24

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: MISC\_FEATURE

LOCATION: (19)..(19)

OTHER INFORMATION: any amino acid residue

US-10-363-369-5

Query Match 100.0%; Score 83; DB 15; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSEGDFLAEGGVR 16  
 Db 1 ADSEGDFLAEGGVR 16

RESULT 12

US-10-363-369-6

Sequence 6, Application US/10363369

Publication No. US2004003157A1

GENERAL INFORMATION:

APPLICANT: Biocata Limited

TITLE OF INVENTION: Anti-Angiogenic Peptides

FILE REFERENCE: P38123WO

CURRENT APPLICATION NUMBER: US/10/363,369

CURRENT FILING DATE: 2003-06-23

PRIOR APPLICATION NUMBER: 0021475.9

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 24

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: MISC\_FEATURE

LOCATION: (23)..(23)

OTHER INFORMATION: OTHER INFORMATION:

FEATURE: NAME/KEY: MISC\_FEATURE

LOCATION: (23)..(23)

OTHER INFORMATION: X = any amino acid

US-10-363-369-6

Query Match 100.0%; Score 83; DB 15; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSEGDFLAEGGVR 16  
 Db 1 ADSEGDFLAEGGVR 16

RESULT 13

US-10-404-568-1

Sequence 1, Application US/1084568

Publication No. US20040248194A1

GENERAL INFORMATION:

APPLICANT: Garcia-Echeverria, Carlos

APPLICANT: Lewis, Claire

TITLE OF INVENTION: Peptide Screen

FILE REFERENCE: 4-2520A/3230/361

CURRENT APPLICATION NUMBER: US/10/484,568

CURRENT FILING DATE: 2004-01-22

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 24

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: MISC\_FEATURE

LOCATION: (23)..(23)

OTHER INFORMATION: OTHER INFORMATION:

FEATURE: NAME/KEY: MISC\_FEATURE

LOCATION: (23)..(23)

OTHER INFORMATION: X = any amino acid

US-10-404-568-3

Query Match 100.0%; Score 83; DB 17; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSEGDFLAEGGVR 16  
 Db 1 ADSEGDFLAEGGVR 16

RESULT 15

US-10-404-568-10

Sequence 10, Application US/10484568

; Publication No. US20040249194A1  
; GENERAL INFORMATION:  
; APPLICANT: Garcia-Bcheverria, Carlos  
; APPLICANT: Lewis, Claire  
; APPLICANT: Robinson, Jeffrey  
; TITLE OF INVENTION: Peptide Screen  
; FILE REFERENCE: 4-32520A/3236/361  
; CURRENT APPLICATION NUMBER: US10/484,568  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 10  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; OTHER INFORMATION: X = any amino acid  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (22)-(22)  
; OTHER INFORMATION: X = any amino acid

US-10-484-568-10

Query Match 100.0%; Score 83; DB 17; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ADSGEGDFLAGGGVR	16
Db	1	ADSGEGDFLAGGGVR	16

Search completed: January 21, 2005, 09:34:36  
Job time : 76 Secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:52 ; Search time 23 Seconds

Post-processing: Maximum Match 0% ; (without alignments)  
Maximum DB seq length: 200000000

Title: US-09-845-765-1

Perfect score: 83  
Sequence: 1 ADSGEGDFLAGGGGVR 16Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% ; Listing First 45 summaries

Database : PIR 79.\*

1: pix1: \*  
2: pix2: \*  
3: pix3: \*  
4: pix4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	83	100.0	644	1 FGHUA fibrinogen alpha chain precursor, short splice form [validated] - human
2	83	100.0	866	2 D44234 fibrinopeptide A -
3	80	96.4	16	2 A229501 fibrinogen alpha C
4	80	96.4	16	2 A229501 fibrinogen alpha C
5	80	96.4	16	2 A24180 fibrinogen alpha C
6	80	96.4	16	2 B28854 fibrinopeptide A -
7	80	96.4	16	2 C28854 fibrinopeptide A -
8	80	96.4	16	2 A28854 fibrinopept ide A -
9	62	74.7	16	2 H229501 fibrinopeptide A -
10	61	73.5	16	2 G229501 fibrinopeptide A -
11	60	72.3	28	2 A05296 fibrinogen alpha C
12	58	69.9	19	2 B229501 fibrinopeptide A -
13	58	69.9	311	2 A05294 fibrinogen alpha C
14	57	68.7	15	2 P229501 fibrinopept ide A -
15	55	66.3	17	2 E229501 fibrinopeptide A -
16	55	66.3	19	2 C229501 fibrinopeptide A -
17	54	65.1	15	2 I229501 fibrinopeptide A -
18	46	55.4	223	2 B96506 fibrinopeptide A -
19	44	53.0	518	2 A13534 fibrinopeptide A -
20	44	53.0	274	2 G72685 fibrinopeptide A -
21	44	53.0	669	2 A72718 fibrinopeptide A -
22	43	51.8	278	2 S225355 fibrinopeptide A -
23	43	51.8	692	1 S57592 fibrinopeptide A -
24	42.5	51.2	15	2 J229506 hypothetical prote
25	42	50.6	15	2 JPF0101 type 4 fibrillar bi
26	42	50.6	144	2 H84434 probable alanyl-tR
27	42	50.6	168	2 T07146 hypothetical prote
28	42	50.6	602	1 GRBPT4 probable phosphos
29	42	50.6	629	2 B75330 probable binding p

## ALIGNMENTS

## RESULT 1

FGHUA fibrinogen alpha chain precursor, short splice form [validated] - human  
N;Alternate names: coagulation factor I  
N;Contains: fibrinopeptide A

C;Species: Homo sapiens (man)

C;Datt: 24-Apr-1984 #sequence revision 30-Jun-1987 #text change 09-Jul-2004

C;Accession: A93956; A37568; A90668; I84456; A44234; C44234; B94433; A90433; B94309; S19

R;Kant, J.A.; Lord, S.T.; Crabtree, G.R.

PROC. NATL. ACAD. SCI. U.S.A. 80, 3953-3957, 1983

A;Title: Partial mRNA sequences for human Alpha, Beta, and gamma fibrinogen chains: evr

A;Reference: A93956; MUID:9134740; PMID:2105623

A;Accession: A93956; MUID:9134740; PMID:2105623

A;Residues: 1-644 &lt;RAN&gt;

A;Cross-references: UNIPROT:P02671; GB:J00128; NID:918245; PID:AA52427\_1; PID:182426

A;Note: the authors translated the codon GAG for residue 247 as GLY, GGA for residue 438

R;Chung, D.W.; Harris, J.E.; Davie, E.W.

Adv. Exp. Med. Biol. 281, 39-48, 1990

A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.

A;Reference number: A43568; MUID:9134740; PMID:2105623

A;Accession: A43568

A;Molecule type: DNA

A;Residues: 1-330, 'A'-332-644 &lt;CTHU&gt;

A;Cross-references: GB:M64982; NID:9458553; PID:AAA17055.1; PID:9458554

R;Rixon, M.W.; Chan, W.Y.; Davie, E.W.; Chung, D.W.

Biochemistry 22, 3237-3244, 1983

A;Title: Characterization of a complementary deoxyribonucleic acid coding for the alpha

A;Reference number: A90468; MUID:83283432; PMID:6688355

A;Accession: A90468

A;Molecule type: mRNA

A;Residues: 1-330, 'A'-332-629 &lt;RIX&gt;

A;Cross-references: GB:J00127; NID:9182423; PID:AA52426\_1; PID:9182424

R;Inam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.

Nucleic Acids Res. 11, 7427-7434, 1983

A;Title: Isolation and characterization of cDNA clones for the Alpha- and Gamma-chains

A;Reference number: 137393; MUID:8406977; PMID:6689067

A;Accession: 184456

A;Status: translated

A;Molecule type: mRNA

A;Residues: 110-156 &lt;RES&gt;

A;Cross-references: GB:K02272; NID:9182427; PID:AA52428\_1; PID:9182428

R;Fu, Y.; Weissenbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redmar

Biochemistry 31, 11968-11972, 1992

A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel

A;Reference number: A44234; MUID:93090725; PMID:1457396

A;Accession: A44234

A;Molecule type: mRNA

A;Residues: 1-51 &lt;PU1&gt;

A;Cross-references: GB:M64982; NID:9458553; PID:AAA17055.1; PID:9458554

A;Accession: C44234

A;Note: sequence extracted from NCBI backbone (NCBIN119912, NCBIN119914, NCBIP1:119918)

A;Accession: C44234

translation initia  
hypothetical prote  
hemolysin A - Esch  
T-cell receptor J-  
pathogenesis-relat  
dimethylallyltrans  
hypothetical prote  
hypothetical prote  
hypothetical prote  
2-oxoacid ferredox  
hypothetical prote  
hypothetical prote  
conserved hypothet  
long-chain fatty a  
hypothetical prote

A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 605-644 <P#2>  
 A;Cross-references: GB:M64982; NID:9458553; PID:AAA17055\_1; PID:9458554  
 A;Note: sequence extracted from NCBI backbone (NCBIP111920)  
 R;Henschen, A.; Lottspeich, F.; Southan, C.; Toft-Petersen, E.  
 in Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe  
 A;Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v  
 A;Accession: B94433  
 A;Molecule type: Protein  
 A;Residues: 20-214; 'RS', 217-298, 'G', 300-303, 'G', 305-629 <HBN>  
 R;Watt, K.W.; Cottrell, B.A.; Strong, D.D.; Doolittle, R.F.  
 Biochemistry 18, 5410-5416, 1979  
 A;Title: Amino acid sequences studies on the alpha chain of human fibrinogen. Overlapping  
 A;Reference number: A94433; MUID:80088231; PMID:518846  
 A;Contents: disulfide bonds  
 A;Accession: A94433  
 A;Molecule type: protein  
 A;Residues: 20-146, 'Q', 148-195, 'N', 197-230, 'N', 232-316, 'SG', 319-406, 'D', 408, 'N', 410-629  
 R;Blomback, B.; Hessel, B.; Hogg, D.  
 Thromb. Res. 8, 639-658, 1976  
 A;Title: Disulfide bridges in NH<sub>2</sub>-terminal part of human fibrinogen.  
 A;Reference number: S19297; MUID:622080; PMID:936108  
 A;Accession: B94309  
 A;Contents: variant, and disulfide bonds  
 A;Accession: B94309  
 A;Molecule type: protein  
 A;Residues: 20-65, 'T', 67-629 <BL0>  
 R;Dewey, R.S.; Liesch, J.M.; Williams, H.R.; Sugg, E.E.; Dolan, C.A.; Davies, P.; Mumford,  
 Bloch, J., 519-524, 1992  
 A;Title: Purification and characterization by fast-atom-bombardment mass spectrometry of  
 incubation with calcium ionophore A23187.  
 A;Reference number: S19297; MUID:92143822; PMID:1736899  
 A;Accession: S19297  
 A;Molecule type: protein  
 A;Residues: 20-40 <DEW>  
 R;Rettig, A.D.; Markland Jr., F.S.  
 Thromb. Res. 52, 541-552, 1989  
 A;Title: A direct-acting fibrinolytic enzyme from the venom of Agkistrodon contortrix co  
 A;Reference number: A60905; MUID:89162316; PMID:3232124  
 A;Accession: A60905  
 A;Molecule type: protein  
 A;Residues: 433-451 <REM>  
 R;Presto, L.J.; Ferguson, E.W.; Steinman, H.M.; McKee, P.A.  
 J. Biol. Chem. 253, 2184-2195, 1978  
 A;Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin.  
 A;Reference number: A92255; MUID:7813008; PMID:632262  
 A;Contents: annotation; cross-linking acceptor sites  
 R;Cottrell, B.A.; Strong, D.D.; Watt, K.W.K.; Doolittle, R.F.  
 Biochemistry 18, 5405-5410, 1979  
 A;Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Exact locat  
 A;Reference number: A90132; MUID:80088230; PMID:518845  
 A;Contents: annotation; cross-linking acceptor sites  
 R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.  
 Ann. N. Y. Acad. Sci. 408, 28-43, 1983  
 A;Title: Covalent structure of fibrinogen.  
 A;Reference number: A90037; MUID:83254370; PMID:6575689  
 A;Contents: annotation; review; disulfide bonds  
 R;Itarte, E.; Plana, M.; Gusach, M.D.; Mario, C.  
 Bichem. Biophys. Res. Commun. 117, 631-636, 1983  
 A;Title: Phosphorylation of fibrinogen by casein kinase 1.  
 A;Reference number: A90116; MUID:84104274; PMID:6318767  
 A;Contents: annotation; phosphorylation  
 A;Note: about one-third of alpha chain molecules in blood were found to be phosphorylate  
 R;Doolittle, R.F.  
 Ann. Rev. Biochem. 53, 195-229, 1984  
 A;Title: Fibrinogen and fibrin.  
 A;Reference number: A90041; MUID:84305751; PMID:6383194  
 A;Contents: annotation; review; EM structure; polymerization, ligands  
 R;Kimura, S.; Aoki, N.  
 J. Biol. Chem. 261, 15591-15595, 1986  
 A;Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.  
 A;Reference number: A92565; MUID:87057190; PMID:2877981

A;Contents: annotation; cross-linking site for alpha-2-plasmin inhibitor.  
 R;Krishnamurthy, S.; Pickens, T.A.; Patel, I.; Wheeler-Jones, C.P.D.; Kakkar, V.V.  
 Biochem. Biophys. Res. Commun. 163, 1256-1264, 1989  
 A;Title: The fibrinogen-derived peptide (RGDS) prevents proteolytic degradation of prote  
 A;Reference number: A33261; MUID:8932031; PMID:2783136  
 A;Contents: annotation; activity of cell attachment (R-G-D) motif  
 R;Kirschbaum, N.B.; Budzynski, A.Z.  
 J. Biol. Chem. 265, 13669-13676, 1990  
 A;Reference number: A7117; MUID:90317977; PMID:2143188  
 A;Contents: annotation; hemein cleavage site  
 A;Note: hemein, a protease from Haemadipsa ghilianii, the giant South American leech,  
 R;Staender, L.; Sillard, R.; Bansch, K.W.; Ruf, A.; Raida, M.; Schulz-Knappe, P.; Schep  
 Biochem. Biophys. Res. Commun. 215, 896-902, 1995  
 A;Title: In vivo degradation of human fibrinogen A alpha: Detection of cleavage sites an  
 A;Reference number: J64334; MUID:96027996; PMID:748058  
 A;Contents: annotation; composition and amino-terminal sequences of carboxyl end peptides  
 C;Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated.  
 C;Comment: The alpha chain binds to 2-4 cross-links to the amino end of fibronectin.  
 C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave  
 C;Complex: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili  
 C;Comment: annotation; composition and amino-terminal sequences of carboxyl end peptides  
 C;Comment: All fibrinogen chains are synthesized in the liver.  
 C;Function:  
 C;Genetics:  
 A;Gene: GDB:FCA  
 A;Cross-references: GDB:119129; OMIM:134820  
 A;Map position: 4q28-qg28  
 A;Introns: 18/3; 60/3; 122/1; 171/2  
 A;Note: the list of introns is incomplete  
 C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha, beta (see t  
 ins are contained in the core. Two three-chain coiled coils emerge from this core and cor  
 from the distal domain nodes.  
 C;Function:  
 A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into f  
 A;Pathway: blood coagulation  
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology  
 C;Keywords: alternative splicing; blood coagulation; coiled coil; glycoprotein; liver; pt  
 F;1-19(Domain: signal sequence #status predicted <SG>  
 F;20-629(Region: cell attachment (R-G-D) motif  
 F;20-35(Region: fibrinopeptide A #status experimental <APT>  
 F;36-629(Region: fibrin alpha chain #status experimental <FGA>  
 F;47(Domain: polymerization site, binding to the distal domain of the gamma chain of &  
 F;51-185(Domain: fibrinogen disulfide ring homology <FDR>  
 F;591-593(Region: cell attachment (R-G-D) motif  
 F;22,460(Binding site: phosphate (Ser) (covalent) #status experimental  
 F;35-36(Cleavage site: Arg-Gly (thrombin) #status experimental  
 F;47(Disulfide bonds: interchain (to alpha-47) #status experimental  
 F;55(Disulfide bonds: interchain (to beta-95) #status experimental  
 F;64(Disulfide bonds: interchain (to gamma-49) #status experimental  
 F;68(Disulfide bonds: interchain (to beta-106) #status experimental  
 F;180(Disulfide bonds: interchain (to gamma-165) #status experimental  
 F;84(Disulfide bonds: interchain (to beta-223) #status experimental  
 F;288,419(Binding site: carbohydrate (Asn) (covalent) #status absent  
 F;322(Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #  
 F;347,385(Cross-link: isopeptide (Gln) (interchain to Lys N6 amino of alpha) #status exp  
 F;527,558,575,581,599(Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status I  
 Query Match 1 ADSGEGDFLAEGGGVR 16  
 Matches 20 ABSGEGDFLAEGGGVR 35  
 RESULT 2  
 D4234  
 fibrinogen alpha chain precursor, extended splice form - human  
 N;Alternate names: coagulation factor I

N;Contains: fibrinopeptide A  
 C;Species: Homo sapiens (man)  
 C;Date: 10-Jun-1993 #sequence\_revision 06-sep-1996 #text\_change 09-Jul-2004  
 C;Accession: D44234; BA4234  
 R;Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma  
 Bloch, Chemistry 31: 11968-11972, 1992.  
 A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove  
 A;Reference number: A44234; MUID:93090725; PMID:1457396  
 A;Accession: D44234  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA; DNA  
 A;Residues: 605-866 <FNU>  
 A;Cross-references: UNIPROT:p02611; GB:MS869; NID:g182406; PID:g182407  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are show  
 C;Comment: The conversion of fibrinogen to fibrin is triggered by the soft clot  
 C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabil  
 C;Comment: All fibrinogen chains are synthesized in the liver.  
 C;Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is  
 C;Genetics:  
 C;Gene: GDB:FGA  
 A;Cross-references: GDB:119129; OMIM:134820  
 A;Intron position: 4q28-4q28  
 A;Map position: 18/3; 60/3; 122/1; 171/2  
 A;Note: the list of introns is incomplete  
 C;Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentical  
 chains in the core. Two three-chain coiled coils emerge from this core and connect it to  
 distal domain nodes.  
 C;Function:  
 A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into  
 A;Pathway: blood coagulation  
 C;Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma  
 C;Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein  
 F;1-19/Domain: signal sequence #status predicted <SIC>  
 F;20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <APR>  
 F;36-863/Product: fibrinopeptide A #status experimental <APR>  
 F;57-185/Domain: fibrinogen disulfide ring homology <PDR>  
 F;591-593/Region: cell attachment (R-G-D) motif  
 F;629-863/Domain: fibrinogen beta/gamma homology <FBG>  
 F;22-460/Binding site: phosphate (Ser) (covalent) #status experimental  
 F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental  
 F;47-/disulfide bonds: interchain (to alpha-47) #status experimental  
 F;55-/disulfide bonds: interchain (to beta-95) #status experimental  
 F;64-/disulfide bonds: interchain (to gamma-49) #status experimental  
 F;68-/disulfide bonds: interchain (to beta-106) #status experimental  
 F;180-/disulfide bonds: interchain (to gamma-165) #status experimental  
 F;184-/disulfide bonds: interchain (to beta-223) #status experimental  
 F;288-/419/Binding site: carbohydrate (Asn) (covalent) #status absent  
 F;322-/Cross-link: isopeptide (Lys) (interchain to Gin-41 of alpha-2-plasmin inhibitor) #  
 F;347-/385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp  
 F;461-/491/Disulfide bonds: #status experimental  
 F;527-/558, 575, 581, 599/Cross-link: isopeptide (Lys) (interchain to Gin of alpha) #status  
 F;686-/831/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 83; DB 2; Length 866;  
 Best local Similarity 100.0%; Pred. No. 4.6e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSGEGDFLAEKKGR 16  
 Db 20 ADSGGEDFLAEKKGR 35

RESULT 3  
 A29501 fibrinopeptide A - baboon

C;Species: Papio sp. (baboon)  
 C;Date: 21-Nov-1987 #sequence\_revision 21-Nov-1987 #text\_change 26-Jan-1996  
 C;Accession: A29501  
 R;Blombeck, B.; Blombeck, M.; Hann, C.  
 unpublished results, cited by Blombeck, B., and Blombeck, M., in Chemotaxonomy and Ser  
 A;Accession: A29501  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-16 <BLO>  
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology  
 Query Match 96.4%; Score 80; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 2.2e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSGEGDFLAEKKGR 16  
 Db 1 ADTGGEDFLAEKKGR 16

RESULT 4  
 B24180 fibrinogen alpha chain - red guenon (fragment)  
 N;Contains: fibrinopeptide A (red guenon, hussar)  
 C;Species: Erythrocebus patas (red guenon, hussar)  
 C;Date: 05-Jun-1988 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
 C;Accession: B24180  
 R;Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. 97, 1487-1492, 1985  
 A;Title: Fibrinopeptides A and B of Japanese monkey (*Macaca fuscata*) and patas monkey (E  
 unenous, and baboons).  
 A;Reference number: A91990; MUID:85289140; PMID:392610  
 A;Accession: B24180  
 A;Molecule type: protein  
 A;Residues: 1-16 <NAK>  
 A;Cross-references: UNIPROT:P12803  
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology  
 Query Match 96.4%; Score 80; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 2.2e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSGEGDFLAEKKGR 16  
 Db 1 ADTGGEDFLAEKKGR 16

RESULT 5  
 A24180 fibrinogen alpha chain - Japanese macaque (fragment)  
 N;Contains: fibrinopeptide A  
 C;Species: Macaca fuscata (Japanese macaque)  
 C;Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 09-Jul-2004  
 C;Accession: A24180  
 R;Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. 97, 1487-1492, 1985  
 A;Title: Fibrinopeptides A and B of Japanese monkey (*Macaca fuscata*) and patas monkey (E  
 unenous, and baboons).  
 A;Reference number: A91990; MUID:85289140; PMID:392610  
 A;Accession: A24180  
 A;Molecule type: protein  
 A;Residues: 1-16 <NAK>  
 A;Cross-references: UNIPROT:P12803  
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology  
 Query Match 96.4%; Score 80; DB 2; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 2.2e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSGEGDFLAEKKGR 16  
 Db 1 ADTGGEDFLAEKKGR 16

RESULT 6  
B28854  
C;Species: Papio hamadryas (hamadryas baboon)  
C;Accession: B28854  
C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 09-Jul-2004  
C;Species: Halichoerus grypus (gray seal)  
C;Accession: H22501  
C;Species: Halichoerus grypus (gray seal)  
C;Accession: H22501  
C;Date: 21-Nov-1987 #sequence\_revision 21-Nov-1987 #text\_change 09-Jul-2004  
J. Biochem. 94, 1973-1978, 1983  
A;Title: Fibronopeptides A and B of baboons (*Papio anubis*, *Papio hamadryas*, and Theropithecus)  
A;Reference number: A91973; MUID:84161822; PMID:6423621  
A;Accession: B28854  
A;Molecule type: protein  
A;Residues: 1-16 <NAK>  
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology  
Query Match 96.4%; Score 80; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.2e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ADSGEGDFLAEQQYR 16  
Db 1 ADTGEGRGDFLAEQQYR 16

RESULT 7  
C28854  
C;Species: Theropithecus gelada (gelada baboon)  
C;Accession: C28854  
C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 09-Jul-2004  
C;Species: *T. gelada* (gelada baboon)  
R.Nakamura, S.; Takenaka, O.; Takahashi, K.  
J. Biochem. 94, 1973-1978, 1983  
A;Title: Fibronopeptides A and B of baboons (*Papio anubis*, *Papio hamadryas*, and Theropithecus)  
A;Reference number: A91973; MUID:84161822; PMID:6423621  
A;Accession: C28854  
A;Molecule type: protein  
A;Residues: 1-16 <NAK>  
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology  
Query Match 96.4%; Score 80; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.2e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ADSGEGDFLAEQQYR 16  
Db 1 ADTGEGRGDFLAEQQYR 16

RESULT 8  
A28854  
C;Species: Papio anubis; *Papio hamadryas anubis* (olive baboon)  
C;Accession: A28854  
C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 09-Jul-2004  
R.Nakamura, S.; Takenaka, O.; Takahashi, K.  
J. Biochem. 94, 1973-1978, 1983  
A;Title: Fibronopeptides A and B of baboons (*Papio anubis*, *Papio hamadryas*, and Theropithecus)  
A;Reference number: A91973; MUID:84161822; PMID:6423621  
A;Molecule type: protein  
A;Residues: 1-16 <NAK>  
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology  
Query Match 96.4%; Score 80; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.2e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ADTGEGRGDFLAEQQYR 16  
Db 1 ADTGEGRGDFLAEQQYR 16

RESULT 9  
H22501  
C;Species: Halichoerus grypus (gray seal)  
C;Accession: H22501  
R.Bombeck, B.; Blommaack, M.; Hann, C.  
unpublished results, cited by Blommaack, B., and Blommaack, M., in Chemotaxonomy and Serological Relationships of Carnivores, Vol. 1, Academic Press, San Diego, CA, 1987, p. 103  
A;Reference number: A29501  
A;Accession: H22501  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <BL0>  
A;Cross-references: UNIPROT:P12803  
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; Fibrinogen disulfide ring homology  
Query Match 74.7%; Score 62; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 0.0015; 2; Mismatches 2; Indels 0; Gaps 0;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 DSGGGDFLAEQQYR 16  
Db 2 DTKESEDFLAEQQYR 16

RESULT 10  
G29501  
C;Species: Theropithecus gelada (gelada baboon)  
C;Accession: G29501  
C;Date: 21-Nov-1987 #sequence\_revision 08-Jun-1990 #text\_change 09-Jul-2004  
C;Species: *T. gelada* (gelada baboon)  
R.Bombeck, B.; Blommaack, M.; Hann, C.  
unpublished results, cited by Blommaack, B., and Blommaack, M., in Chemotaxonomy and Serological Relationships of Carnivores, Vol. 1, Academic Press, San Diego, CA, 1987, p. 103  
A;Reference number: A29501  
A;Accession: G29501  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <BL0>  
A;Cross-references: UNIPROT:Q7M3J7  
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide ring homology  
Query Match 73.5%; Score 61; DB 2; Length 16;  
Best Local Similarity 73.3%; Pred. No. 0.0021; 2; Mismatches 2; Indels 0; Gaps 0;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 DSGGGDFLAEQQYR 16  
Db 2 DGKEGEFFIAEQQYR 16

RESULT 11  
A0296  
C;Species: Canis lupus familiaris (dog)  
C;Accession: A94308; A03118; A37511; A05266; B37511; C03118  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
R.Birken, S.; Wilmer, G.D.; Canfield, R.E.  
A;Title: Studies of the structure of canine fibrinogen.  
A;Reference number: A94308; MUID:76081726; PMID:1198547  
A;Accession: A94308  
A;Molecule type: protein  
A;Residues: 1-28 <BL0>  
A;Cross-references: UNIPROT:P02673  
R.Bombeck, B.; Blommaack, M.; Groendahl, N.J.  
Acta Chem. Scand. 19, 1789-1791, 1965  
A;Title: Studies on fibrinopeptides from mammals.  
A;Reference number: A03118  
A;Accession: A03118

A;Molecule type: protein  
A;Residues: I-16 <BLO>  
R.Osbahr Jr., A.J.; Colman, R.W.; Laki, K.; Gladner, J.A.  
Biochem. Biophys. Res. Commun. 14, 555-558, 1964  
A;Reference number: A37511; MUID:66020594; PMID:5836555  
A;Accession: A37511  
A;Molecule type: protein  
A;Residues: I,D,3,'E<sup>KQ</sup>',8-16 <OSB>  
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology  
C;Keywords: blood coagulation; liver; phosphoprotein; plasma  
F1-16/Product: fibrinopeptide A #status experimental <APT>  
F1-16/Product: fibrinopeptide A #status experimental <APT>  
Query Match 72.3%; Score 60; DB 2; Length 28;  
Best Local Similarity 73.3%; Pred. No. 0.0055; Mismatches 1; Indels 0; Gaps 0;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 DSGEGDFLAEGGV 16  
Db 2 NSKEGEFIAGGGVR 16

RESULT 12  
B29501  
fibrinopeptide A - European moose  
C;Species: Alces alces alces (European moose, elk)  
C;Date: 21-Nov-1987 #sequence\_revision 21-Nov-1987 #text\_change 09-Jul-2004  
C;Accession: B29501  
R.Bloombaek, B.; Bloombaek, M.; Hann, C.  
unpublished results, cited by Bloombaek, B., and Bloombaek, M., in Chemotaxonomy and Ser  
A;Reference number: A29501  
A;Accession: B29501  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <BLO>  
A;Cross-references: UNIPROT:Q7MB35  
C;Superfamily: fibrinogen beta chain; fibrinogen gamma homology; fibrinogen disulf  
Query Match 69.9%; Score 58; DB 2; Length 19;  
Best Local Similarity 69.8%; Pred. No. 0.0076; Mismatches 1; Indels 0; Gaps 0;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 ADSGEGDFLAEGGV 16  
Db 4 SDPAGGEFLAEGGV 19

RESULT 13  
A05294  
Fibrinogen alpha chain - bovine (fragments)  
N;Contains: fibrinopeptide A  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 05-Jun-1987 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
C;Accession: A05294; A20717; A37505; A37506; A37507; B37505; C03117  
R.Henschen, A.; Lottspeich, F.; Topfer-Petersen, E.; Kahl, M.; Timpl, R.  
in Proteins of the Biological Fluids, Proc. 28th Colloq., ed. Peeters, H., pp. 47-50, Per  
A;Reference number: A05294  
A;Accession: A05294  
A;Molecule type: protein  
A;Residues: 1-28-49-55-80-81-108 <HEN>  
A;Cross-references: UNIPROT:P02672  
R.Chung, D.W.; Rixon, M.W.; Davie, E.W.  
in Proteins in Biology and Medicine, Bradshaw, R.A., ed., pp.309-328, Academic Press, Ne  
A;Title: The biosynthesis of fibrinogen and the cloning of its cDNA.  
A;Reference number: A25715  
A;Accession: A25715  
A;Molecule type: mRNA  
A;Residues: 109-311 <CHU>  
R.Sjogquist, J.; Blomback, B.; Wallen, P.  
Ark. Kem. 16, 425-436, 1960  
A;Title: Amino acid sequence of bovine fibrinopeptides.  
A;Reference number: A03117  
A;Accession: A03117

RESULT 14  
F29501  
fibrinopeptide A - wombat  
C;Species: Vombatidae gen. sp. (wombat)  
C;Date: 21-Nov-1987 #sequence\_revision 08-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: F29501  
R.Bloombaek, B.; Bloombaek, M.; Hann, C.  
unpublished results, cited by Bloombaek, B., and Bloombaek, M., in Chemotaxonomy and Ser  
A;Reference number: A29501  
A;Accession: F29501  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <BLO>  
A;Cross-references: UNIPROT:Q7MB35  
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology  
Query Match 69.7%; Score 57; DB 2; Length 15;  
Best Local Similarity 69.8%; Pred. No. 0.0085; Mismatches 1; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 5 EGDFLAEGGV 16  
Db 4 EGDFLAEGGV 15

RESULT 15  
B29501  
fibrinopeptide A - pig  
C;Species: Sus scrofa domesticus (domestic pig)  
C;Date: 21-Nov-1987 #sequence\_revision 21-Nov-1987 #text\_change 09-Jul-2004  
C;Accession: B29501  
R.Bloombaek, B.; Bloombaek, M.; Hann, C.  
unpublished results, cited by Bloombaek, B., and Bloombaek, M., in Chemotaxonomy and Ser  
A;Reference number: A29501  
A;Accession: B29501  
A;Molecule type: protein

A: Residues: 1-17 <BLO>  
A,Cross-references: UNIPROT:P14460  
R,Bloemberg, B.; Blomberg, M.; Groendahl, N.J.  
Acta Chem. Scand. 19, 1789-1791, 1965  
A>Title: Studies on fibrinopeptides from mammals.  
A:Reference number: A03118  
A:Contents: annotation; confirmation of species assignment  
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide-linked fragments  
Query Match 66.3%; Score 55; DB 2; Length 17;  
Best Local Similarity 83.3%; Pred. No. 0.02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	5	EGDFLAEGGWR	16
	:		
Db	6	KGEFLAEGGGWR	17

Search completed: January 21, 2005, 08:31:39  
Job time : 27 secs

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GenCore version 5.1.6

January 21, 2005, 08:04:52 ; Search time 91 Seconds

(without alignments)

101.165 Million cell updates/sec

### OM protein - protein search, using sw model

Run on: January 21, 2005, 08:04:52 ; Search time 91 Seconds

(without alignments)

Title: US-09-845-765-1

Perfect score: 83

Sequence: 1 ADSGEGDFLAEGGV R 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database : UniProt 02:  
1: uniprot\_sprot:  
2: uniprot\_trembl:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	83	100.0	218	2 Q8WW76	Q8WW76 homo sapien
2	83	100.0	289	2 Q6NSDB	Q6NSDB homo Sapien
3	83	100.0	289	2 AAH70246	AAH70246 homo sapi
4	83	100.0	866	1 FIBA_HUMAN	FIBA_HUMAN
5	80	96.4	16	1 FIBA_MACFU	FIBA_MACFU
6	76	91.6	16	1 FIBA_HYLLA	FIBA_HYLLA
7	71	85.5	16	1 FIBA_MANLE	FIBA_MANLE
8	65	78.3	18	1 FIBA_CAMDR	FIBA_CAMDR
9	64	77.1	19	1 FIBA_BISB	FIBA_BISB
10	62	74.7	15	1 FIBA_SYNCA	FIBA_SYNCA
11	62	74.7	16	1 FIBA_CERSI	FIBA_CERSI
12	62	74.7	16	2 Q7m316	Q7m316 halichoerus
13	61	73.5	15	2 Q7m317	Q7m317 ursus sp. (
14	61	73.5	18	1 FIBA_LAMGL	FIBA_LAMGL
15	60	72.3	28	1 FIBA_CANFA	FIBA_CANFA
16	59	71.1	16	1 FIBA_FELCA	FIBA_FELCA
17	59	71.1	16	1 FIBA_TAPTE	FIBA_TAPTE
18	59	71.1	19	1 FIBA_BUBBL	FIBA_BUBBL
19	58	69.9	16	1 FIBA_ODOHE	FIBA_ODOHE
20	58	69.9	19	1 FIBA_CEREL	FIBA_CEREL
21	58	69.9	19	2 QM315	QM315 canis famili
22	58	69.9	596	2 FIBA_BOVIN	FIBA_BOVIN
23	57	68.7	15	2 QM318	QM318 bombyidae
24	56	67.5	19	1 FIBA_MUNMU	FIBA_MUNMU
25	55	66.3	17	1 FIBA_PIG	FIBA_PIG
26	55	66.3	19	1 FIBA_SHEEP	FIBA_SHEEP
27	54	65.1	15	2 QM319	QM319 macropus sp
28	54	65.1	16	1 FIBA_EQVAS	FIBA_EQVAS
29	54	65.1	19	1 FIBA_CERNI	FIBA_CERNI
30	53	63.9	14	1 FIBA_HORSE	FIBA_HORSE
31	52	62.7	557	2 Q99K47	Q99K47 mus musculu

RESULT	1	PRELIMINARY;	PRT;	218 AA.
ID	Q8WW76			
AC	Q8WW76;			
DT	01-MAR-2002 (TREMBUREL, 20, Last sequence update)			
DT	01-MAR-2002 (TREMBUREL, 20, Last annotation update)			
DE	FGA protein.			
OS	Homo sapiens (Human).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OX			
OU	Mammalia; Buteraria; Primates; Catarrhini; Hominoidea; Homo.			
RN	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	MEDLINE=22388257; PubMed=12477932;			
RA	Straubberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Blatt N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blatt N.K., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soarees M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McKernan R.J., Malek J.A., Gunnatne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Munay D.M., Sodegren E.J., Lu X., Gibbs R.A., Fahay J.J., Heiton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., RA Whiting M., Madan A., Young C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.J., Schmitz J.J., Myers R.M., Butterfield Y.S., Rodriguez M.I., Skalska U., Smailly D.E., Schneich A., Jones S.J., Marra M.A.; RT Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";			
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	RN [2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Straubberg R.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.			
RA	DR EMBL; BC020764; AAH20764.1; -. DR HSSP; P02671; 1F2A. DR SEQUENCE 218 AA; 24695 MN; 36D756A8116BA94A CRC64;			
RA	RA Query Match 100.0%; Score 83; DB 2; Length 218; Best Local Similarity 100.0%; Pred. No. 0_00017; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
RA	OY 1 ADSGEGDFLAEGGV R 16			
Db	20 ADSGEGDFLAEGGV 35			

Q6uu61 oryza sativ  
Aaq56514 oryza sat  
P14462 rangifer ta  
Q9xa0 ipomoea bat  
Q84sas aster tripl  
Q9ccy9 arabidopsis  
O6m066 methanococc  
Ca29861 methanoco  
Q8u287 pyrococcus  
Q8ruj7 helianthus  
Q9a945 oryza sativ  
Q61132 drosophila  
Q6ttt6 ewinia amy  
Q8gfn7 citrobacter

RESULT 2  
 QNSD8 PRELIMINARY; PRT; 289 AA.  
 ID QNSD8 PRELIMINARY; PRT; 289 AA.  
 AC QNSD8; PRELIMINARY; PRT; 289 AA.  
 DT 05-JUL-2004 (TREMBREL\_27, Created)  
 DT 05-JUL-2004 (TREMBREL\_27, Last sequence update)  
 DT 05-JUL-2004 (TREMBREL\_27, Last annotation update)  
 DR FGA protein.  
 GN Name=FGA;  
 OS Homo sapiens (Human);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1] SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE-22380257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Buetow K.H., Moore T., Max S.I., Wang J., Heleb F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Sores M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Crimaci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J.,  
 RA Boak S.A., McEwan P.J., McKernan P.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muñoz D.M., Sodergren E.J., Lu X., Gibbs R.E.J., Lu X., Gibbs R.A.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Crimaci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,  
 RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muñoz D.M., Sodergren E.J., Lu X., Gibbs R.E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA RA Krzywinski M.I., Skalska U., Smilus D.E., Schnurch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Strausberg R.;  
 RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC070246; AAH70246.1; -.  
 SQ SEQUENCE 289 AA; 32991 MW; ICPAECB437F73BA0 CRC64;  
 Query Match 100.0%; Score 83; DB 2; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 0.00022; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADSEGGDFLAEGGAVR 16  
 Db 20 ADSEGGDFLAEGGVR 35

RESULT 3  
 FIBA\_HUMAN STANDARD; PRT; 866 AA.  
 ID FIBA\_HUMAN STANDARD; PRT; 866 AA.  
 AC P02671; Q9BXG2; Q0UCH2;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Fibrinogen alpha/alpha-B chain Precursor [Contains: Fibrinopeptide A].  
 GN Name=FGA;  
 OS Homo sapiens (Human);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1] SEQUENCE FROM N.A. (ISOFORM ALPHA-E).  
 RX MEDLINE=93090725; PubMed=1457396;  
 RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,  
 RA Roy S.N., Redman G.M., Grunenberger G.;  
 RT "Carboxy-terminal-extended variant of the human fibrinogen alpha  
 subunit: a novel exon conferring marked homology to beta and gamma  
 subunits";  
 RT Biochemistry 31:11968-11972 (1992).  
 RN [2] SEQUENCE FROM N.A. (ISOFORM ALPHA-E).  
 RA Chung D.W., Grunenberger G.;  
 RT "Fibrinogen DNA and protein sequences";  
 RT (Eds.) Ebert R.F. (Eds.);  
 RL Index of variant human fibrinogens, pp.13-24, CRC Press, Boca Raton  
 RN (1994).  
 RP SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND  
 RP ALA-456.  
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RA Nickerson D.A.;  
 RT "SeattleSNPs. NHLBI Hu66682 program for genomic applications, UW-  
 FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]

RESULT 4  
 FIBA\_HUMAN STANDARD; PRT; 866 AA.  
 ID FIBA\_HUMAN STANDARD; PRT; 866 AA.  
 AC P02671; Q9BXG2; Q0UCH2;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Fibrinogen alpha/alpha-B chain Precursor [Contains: Fibrinopeptide A].  
 GN Name=FGA;  
 OS Homo sapiens (Human);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1] SEQUENCE FROM N.A. (ISOFORM ALPHA-E).  
 RX MEDLINE=93090725; PubMed=1457396;  
 RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,  
 RA Roy S.N., Redman G.M., Grunenberger G.;  
 RT "Carboxy-terminal-extended variant of the human fibrinogen alpha  
 subunit: a novel exon conferring marked homology to beta and gamma  
 subunits";  
 RT Biochemistry 31:11968-11972 (1992).  
 RN [2] SEQUENCE FROM N.A. (ISOFORM ALPHA-E).  
 RA Chung D.W., Grunenberger G.;  
 RT "Fibrinogen DNA and protein sequences";  
 RT (Eds.) Ebert R.F. (Eds.);  
 RL Index of variant human fibrinogens, pp.13-24, CRC Press, Boca Raton  
 RN (1994).  
 RP SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND  
 RP ALA-456.  
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RA Nickerson D.A.;  
 RT "SeattleSNPs. NHLBI Hu66682 program for genomic applications, UW-  
 FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

- RP SEQUENCE OF 1-655 FROM N.A. (ISOFORM ALPHA-B).  
 RC TISSUE=Liver;  
 RX PMID=9134740; PubMed=2102623;  
 RA Chung D.W., Harris J.E., Davie E.W.;  
 RT "Nucleotide sequences of the three genes coding for human  
 fibrinogen.";  
 RL Adv. Exp. Med. Biol. 281:39-48 (1990).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RX MEDLINE=83247395; PubMed=6575389;  
 RA Kant J.A., Lord S.T., Crabtree G.R.;  
 RT "Partial mRNA sequence for human A alpha, B beta, and gamma  
 fibrinogen chains: evolutionary and functional implications.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).  
 RN [6]  
 RP SEQUENCE OF 1-629 FROM N.A.  
 RX MEDLINE=83283432; PubMed=6688355;  
 RA Dixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;  
 RT "Characterization of a complementary deoxyribonucleic acid coding for  
 the alpha chain of human fibrinogen.";  
 RL Biochemistry 22:3237-3244 (1983).  
 RN [7]  
 RP SEQUENCE OF 20-629.  
 RA Henschel A., Lottspeich F., Southan C., Topfer-Petersen E.;  
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some  
 structural variants.";  
 RL (In) Peeters H. (eds.);  
 RT Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,  
 RL Pergamon Press, Oxford (1980).  
 RN [8]  
 RP SEQUENCE OF 20-629, AND DISULFIDE BONDS.  
 RX MEDLINE=80088231; PubMed=518846;  
 RA Watt K.W.H., Cottrell B.A., Strong D.D., Doolittle R.F.;  
 RT "Amino acid sequence studies on the alpha chain of human fibrinogen.  
 Overlapping sequences providing the complete sequence.";  
 RL Biochemistry 18:5410-5416(1979).  
 RN [9]  
 RP SEQUENCE OF 110-156 FROM N.A.  
 RX MEDLINE=84065777; PubMed=6689067;  
 RA Inman A.M., Eaton M.A., Williamson R., Humphries S.;  
 RT "Isolation and characterisation of cDNA clones for the A alpha- and  
 RT gamma-chains of human fibrinogen.";  
 RL Nucleic Acids Res. 11:7427-7434(1983).  
 RN [10]  
 RP SEQUENCE OF 605-644 FROM N.A. (ISOFORM ALPHA).  
 RX MEDLINE=83253384; PubMed=6575700;  
 RA Chung D.W., Rixon M.W., Que B.G., Davie E.W.;  
 RT "Cloning of fibrinogen genes and their cDNA.";  
 RL Ann. N.Y. Acad. Sci. 408:449-456(1983).  
 RN [11]  
 RP SEQUENCE OF 20-35.  
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;  
 RT "Studies on fibrinopeptides from primates.";  
 RL Acta Chem. Scand. 19:1788-1789(1965).  
 RN [12]  
 RP CROSS-LINKING ACCEPTOR SITES.  
 RX MEDLINE=80089230; PubMed=518845;  
 RA Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;  
 RT "Amino acid sequence studies on the alpha chain of human fibrinogen.  
 Extract location of cross-linking acceptor sites.";  
 RL Biochemistry 18:5405-5410(1979).  
 RN [13]  
 RP CROSS-LINKING ACCEPTOR SITES.  
 RX MEDLINE=78110085; PubMed=632262;  
 RA Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;  
 RT "Localization of the alpha-chain cross-link acceptor sites of human  
 fibrin.";  
 RL J. Biol. Chem. 253:2184-2195(1978).  
 RN [14]  
 RP VARIANT, AND DISULFIDE BONDS.  
 RX MEDLINE=76225080; PubMed=93108;  
 RA Blomback B., Hessel B., Hogg D.;  
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
- RL Thromb. Res. 8:633-658 (1976).  
 RN [15]  
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.  
 RX MEDLINE=84305751; PubMed=6383194;  
 RA Doolittle R.F.;  
 RT "Fibrinogen and fibrin.";  
 RL Annu. Rev. Biochem. 53:195-229(1984).  
 RN [16]  
 RP CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.  
 RX MEDLINE=87057190; PubMed=2877981;  
 RA Kimura S., Aoki N.;  
 RT "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";  
 RL J. Biol. Chem. 261:15591-15595(1986).  
 RN [17]  
 RP PHOSPHORYLATION.  
 RX MEDLINE=84104274; PubMed=6318767;  
 RA Itarte E., Plana M., Glasch M.D., Martos C.;  
 RT "Phosphorylation of fibrinogen by casein kinase 1.";  
 RL Biochem. Biophys. Res. Commun. 117:631-636(1983).  
 RN [18]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.  
 RX MEDLINE=92218459; PubMed=1560020;  
 RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;  
 RT "The structure of residues 7-16 of the A alpha-chain of human  
 fibrinogen bound to bovine thrombin at 2.3-A resolution.";  
 RL J. Biol. Chem. 267:7911-7920(1992).  
 RN [19]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 130-216.  
 RX MEDLINE=97472408; PubMed=9333233;  
 RA Spraggan G., Everse S.J., Doolittle R.F.;  
 RT "Crystal structures of fragment D from human fibrinogen and its  
 crosslinked counterpart from fibrin.";  
 RL Nature 389:455-462(1997).  
 RN [20]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.  
 RX MEDLINE=9829395; PubMed=9628725;  
 RA Everse S.J., Spraggan G., Veerapandian L., Riley M., Doolittle R.F.;  
 RT "Crystal structure of fragment double-D from human fibrin with two  
 different bound ligands.";  
 RL Biochemistry 37:6637-6642(1998).  
 RN [21]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.  
 RX MEDLINE=98356117; PubMed=9889040;  
 RA Spraggan G., Applegate D., Everse S.J., Zhang J.Z., Veerapandian L.,  
 RA Redman C., Doolittle R.F., Griesinger G.;  
 RT "Crystal structure of a recombinant alphaEBC domain from human  
 fibrinogen-420.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:9093-9104(1998).  
 RN [22]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=99175089; PubMed=10074346;  
 RA Everse S.J., Spraggan G., Veerapandian L.,  
 RT "Conformational changes in fragments D and double-D from human  
 fibrinogen) upon binding the peptide ligand GLY-His-Arg-Pro-amide.";  
 RL Biochemistry 38:2941-2946(1999).  
 RN [23]  
 RP VARIANT KYOTO-2.  
 RX MEDLINE=91300049; PubMed=2070049;  
 RA Yoshida N., Okuma M., Hirata M., Matsuda M., Yamazumi K., Asakura S.;  
 RT "Fibrinogen Kyoto II, a new congenitally abnormal molecule,  
 characterized by the replacement of A alpha proline-18 by leucine.";  
 RL Blood 78:149-153(1991).  
 RN [24]  
 RP VARIANT LIMA.  
 RX MEDLINE=92340680; PubMed=1634621;  
 RA Mackawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,  
 RA Takahashi N., Archachan-Pinango C.L., Rodriguez S., Nagy J.,  
 RA Perez-Requejo J.L., Matsuda M.;  
 RT "Fibrinogen Lima: a homozygous dysfibrinogen with an A alpha-arginine-  
 141 to serine substitution associated with extra N-glycosylation at A  
 alpha-sparcine-139. Impaired fibrin gel formation but normal fibrin-  
 facilitated plasminogen activation catalyzed by tissue-type  
 RT plasminogen activator.";

RL	J. Clin. Invest. 90:67-76 (1992).	RL	Acta Chem. Scand. 19:1788-1789 (1965).	
RN	[25]	CC	-1- FUNCTION: Fibrinogen has a double function: yielding monomers that	
RP	VARIANT CARACAS-2.	CC	polymerize into fibrin and acting as a cofactor in platelet	
RX	MEDLINE=91268018; PubMed=1675636;	CC	aggregation.	
RA	Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,	CC	-1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains	
RA	Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,	CC	(alpha, beta and gamma), linked to each other by disulfide bonds.	
RA	Arocha-Pinango C.L., Matsuda M.,	CC	CC	-1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
RT	"An A alpha Ser-434 to N-glycosylated Asn substitution in a	CC	which cleaves fibrinopeptides A and B from alpha and beta chain,	
RT	dystfibrinogen, fibrinogen Caracas II, characterized by impaired fibrin	CC	and thus exposes the N-terminal polymerization sites responsible	
RT	gel formation.";	CC	for the formation of the soft clot.	
RL	J. Biol. Chem. 266:11575-11581 (1991).	DR	PIR; A24180; A24180.	
RN	[26]	DR	PIR; A28654; A28654.	
RP	VARIANT DUSART.	DR	PIR; B24180; B24180.	
RX	MEDLINE=9323289; PubMed=8473507;	DR	PIR; B28654; B28654.	
RA	Koopman J., Haverkate F., Grimmbergen J., Lord S.T., Mobesson M.W.,	DR	PIR; C28654; C28654.	
RA	Cañorizo J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,	KW	Blood coagulation; Direct protein sequencing; Plasma.	
RA	Caen J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,	FT	PEPTIDE 1 16 Fibrinopeptide A.	
RT	"Molecular basis for fibrinogen Dusart (A alpha 554 Arg--Cys) and its	FT	NON TER 16 16	
Query Match	100.0%; Score 83; DB 1; Length 866;	SQ	SEQUENCE 16 AA; 1551 MW; 49EBB63EA04DD3 CRC64;	
Best Local Similarity	100.0%; Pred. No. 0.00067; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match	96.4%; Score 80; DB 1; Length 16;	
QY	1 ADSGEGDFLAEGGGR 16	Best Local Similarity	93.8%; Pred. No. 3.5e-05; Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Db	20 ADSGEGDFLAEGGGR 35	QY	1 ADSGEGDFLAEGGGR 16	
Db	1 ADIGEGDFLAEGGGR 16	Db	1 ADIGEGDFLAEGGGR 16	
RESULT 5				
FIBA_MACFU	STANDARD;	PRT;	16 AA.	
ID	FIBA_MACFU			
AC	P12803;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).			
GN	Name=FGA;			
OS	Macaca fuscata fuscata (Japanese macaque)' (Cynomolgus monkey),			
OS	Macaca fascicularis (Crab eating macaque),			
OS	Macaca mulatta (Rhesus macaque),			
OS	Cercopithecus aethiops (Green monkey) (Grivet),			
OS	Brytoccoebus patas (Red guenon) (Cercopithecus patas),			
OS	Papio anubis (Olive baboon),			
OS	Theropithecus gelada (Galada baboon),			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;			
OC	Cercopithecinae; Macaca.			
OX	NCBI_TaxID=9543, 9541, 9544, 9534, 9538, 9555, 9557, 9565;			
RN	[1]			
RP	SEQUENCE.			
RC	SPECIES=B.patas, and M.fuscata;			
RX	MEDLINE=85289140; PubMed=398610;			
RA	Nakamura S., Takenaka O., Takahashi K.,			
RA	"Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas			
RT	monkey (Brytoccoebus patas); their amino acid sequences, restricted			
RT	mutations, and a molecular phylogeny for macaques, guenons, and			
RT	baboons";			
RL	J. Biochem. 97:1487-1492 (1985).			
RN	[2]			
RP	SEQUENCE.			
RC	SPECIES=B.anubis, P.hamadryas, and T.gelada;			
RX	MEDLINE=84161822; PubMed=6423621;			
RA	Nakamura S., Takenaka O., Takahashi K.,			
RT	"Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,			
RT	and Theropithecus gelada); their amino acid sequences and evolutionary			
RT	rates and a molecular phylogeny for the baboons.";			
RL	J. Biochem. 94:1973-1978 (1983).			
RN	[3]			
RP	SEQUENCE,C.aethiops, M.mulatta, and M.fascicularis;"			
RC	SPECIES=C.aethiops, M.mulatta, and M.fascicularis;"			
RA	"Studies on fibrinopeptides from primates.";			
RT	Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.,			
RT	Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.,			
RESULT 6				
FIBA_HYLIA	STANDARD;	PRT;	16 AA.	
ID	FIBA_HYLIA			
AC	P14453;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).			
GN	Name=FGA;			
OS	Hylobates lar (Common gibbon),			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.			
OX	NCBI_TaxID=9880;			
RN	[1]			
RP	SEQUENCE.			
RC	MEDLINE=70294424; PubMed=5466708;			
RX	Moers G.A., Doolittle R.F.; Roberts B.F.;			
RA	"Gibbon fibrinopeptides: identification of a glycine-serine alleleism			
RT	at position B3,"			
RL	Science 170:468-470 (1970).			
RN	-1- FUNCTION: Fibrinogen has a double function: Yielding monomers that			
CC	polymerize into fibrin and acting as a cofactor in platelet			
CC	aggregation.			
CC	-1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains			
CC	(alpha, beta, and gamma), linked to each other by disulfide bonds.			
CC	-1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,			
CC	which cleaves fibrinopeptides A and B from alpha and beta chains,			
CC	and thus exposes the N-terminal polymerization sites responsible			
CC	for the formation of the soft clot.			
KW	Blood coagulation; Direct protein sequencing; Plasma.			
FT	PEPTIDE 1 16 Fibrinopeptide A.			
FT	NON TER 16 16			
SQ	SEQUENCE 16 AA; 1565 MW; 49EBB63EA04DD3 CRC64;			
Query Match	91.6%; Score 75; DB 1; Length 16;			
Best Local Similarity	87.5%; Pred. No. 0.00014; Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			
QY	1 ADSGEGDFLAEGGGR 16			
Db	1 ADTGEGDFLAEGGGR 16			
RESULT 7				

FIBA\_MANIE STANDARD PRT; 16 AA.

ID FIBA\_MANIE STANDARD PRT; 16 AA.

AC P1455;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DB Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).

GN Name=FGA;

OS Mandrillus leucophaeus (Drill) (*Papio leucophaeus*); Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopithecinae; Mandrillus.

OC NCBI\_TaxID=9568;

OX

RN [1]

RP

RX MEDLINE-69115139; PubMed=4974768;

RA Doolittle R.F.; Glasgow C.; Gross G.A.;

RT "Characterization of fibrinopeptides A and B from a drill (Mandrillus leucophaeus)", *Biochim. Biophys. Acta* 175:217-219(1969).

RL

CC -!- FUNCTION: Fibrinogen has a double function: Yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.

CC -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds. -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.

KW Blood coagulation; Direct protein sequencing; Plasma.

FT PEPTIDE 1 15 Fibrinopeptide A.

FT NON\_TER 16 16 MW: 08E8CBB77BA051A4 CRC64;

SO SEQUENCE 16 AA: 1567

Query Match 85.5%; Score 71; DB 1; Length 16;

Best Local Similarity 75.0%; Pred. No. 0.00082; Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16

Db 1 ADTGDDDFLAEGGGVR 16

RESULT 9

FIBA\_BISBO STANDARD PRT; 19 AA.

ID FIBA\_BISBO STANDARD PRT; 19 AA.

AC P14541;

DT 01-JAN-1990 (Rel. 13, Created)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DB Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).

GN Name=FGA;

OS Bison bonasus (European bison).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Bovinae; Bison.

OX NCBI\_TaxID=9902;

RN [1]

RP

RA Blomback B., Grondahl N.J.;

RT "Studies on fibrinopeptides from mammals.", *Acta Chem. Scand.* 19:1789-1791(1965).

RL

CC -!- FUNCTION: Fibrinogen has a double function: Yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.

CC -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds. -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.

KW Blood coagulation; Direct protein sequencing; Plasma.

FT PEPTIDE 1 19 Fibrinopeptide A.

FT NON\_TER 19 19 MW: 9B455A0F473B59C5 CRC64;

SO SEQUENCE 19 AA: 1836

Query Match 77.1%; Score 64; DB 1; Length 19;

Best Local Similarity 75.0%; Pred. No. 0.01; Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ADSGEGDFLAEGGGVR 16

Db 4 SDPASGDFLAEGGGVR 19

RESULT 10

FIBA\_SYNCA STANDARD PRT; 15 AA.

ID FIBA\_SYNCA STANDARD PRT; 15 AA.

AC P1463;

DT 01-JAN-1990 (Rel. 13, Created)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DB Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).

GN Name=FGA;

OS Syncerus caffer (Cape buffalo).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Bovinae; Syncerus.

CC NCBI\_TaxID=9970;

RN [1]

RP

RA Doolittle R.F., Schubert D., Schwartz S.A.;

RX MEDLINE-67209145; PubMed=6033721;

RP

RX SEQUENCE.

RA Doolittle R.F.; Schubert D.; Schwartz S.A.;

RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I. Dromedary camel, mule deer, and cape buffalo.", *Arch. Biochem. Biophys.* 118:456-467(1967).

RL

CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.

CC -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds. -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.

KW Blood coagulation; Direct protein sequencing; Plasma.

RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.  
 RT Dromedary camel, mule deer, and cape buffalo.";  
 RL Arch. Biochem. Biophys. 118:456-467(1971).  
 CC -!- FUNCTION: Fibrinogen has a double function: Yielding monomers that  
 CC polymerize into fibrin and acting as a cofactor in platelet  
 CC aggregation.

-!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains  
 CC (alpha, beta and gamma), linked to each other by disulfide bonds.  
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,  
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,  
 CC and thus exposes the N-terminal polymerization sites responsible  
 CC for the formation of the soft clot.  
 KW Blood coagulation; Direct protein sequencing; Plasma.  
 FT PEPTIDE 1 15 MW; Fibrinopeptide A.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1480 MW; 4E99BEASF0B41CC6 CRC64;

Query Match 74.7%; Score 62; DB 1; Length 15;  
 Best local Similarity 73.3%; Pred. No. 0.018;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 DSGBEDFLAEGGGVR 16  
 Db 1 BDGSDSFPLAEGGGVR 15

RESULT 11

FIBA_CERST	STANDARD;	PRT;	16 AA.																																																																																																																																																													
ID	Q7M317	PRT;	16 AA.																																																																																																																																																													
AC	P14535;																																																																																																																																																															
DT	01-JAN-1990 (Rel. 13, Last sequence update)																																																																																																																																																															
DT	01-JAN-1990 (Rel. 13, Last annotation update)																																																																																																																																																															
DT	05-JUL-2004 (Rel. 44, Last annotation update)																																																																																																																																																															
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).																																																																																																																																																															
GN	Name=FGA;																																																																																																																																																															
OS	Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).																																																																																																																																																															
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;																																																																																																																																																															
OC	Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.																																																																																																																																																															
OX	NCBI_TaxID=9807;																																																																																																																																																															
RN	[1]																																																																																																																																																															
RP	SEQUENCE.																																																																																																																																																															
RA	O'Neil P.B., Doolittle R.F.;																																																																																																																																																															
RT	"Mammalian phylogeny based on fibrinopeptide amino acid sequences.";																																																																																																																																																															
RL	Syst. Zool. 22:590-595(1973).																																																																																																																																																															
CC	-!- FUNCTION: Fibrinogen has a double function: yielding monomers that																																																																																																																																																															
CC	polymerize into fibrin and acting as a cofactor in platelet																																																																																																																																																															
CC	aggregation.																																																																																																																																																															
-!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains CC (alpha, beta and gamma), linked to each other by disulfide bonds. CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, CC which cleaves fibrinopeptides A and B from alpha and beta chains, CC and thus exposes the N-terminal polymerization sites responsible CC for the formation of the soft clot. KW Blood coagulation; Direct protein sequencing; Plasma. FT PEPTIDE 1 16 MW; Fibrinopeptide A. FT NON TER 16 16 SQ SEQUENCE 16 AA; 1639 MW; 0958CBB6293F4C81 CRC64; <p>Query Match 74.7%; Score 62; DB 1; Length 16;    Best local Similarity 73.3%; Pred. No. 0.019;    Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;</p> <p>RESULT 12</p> <table border="0"> <tr><td>Q7M316</td><td>PRELIMINARY;</td><td>PRT;</td><td>16 AA.</td></tr> <tr><td>ID</td><td>Q7M316</td><td>PRT;</td><td>16 AA.</td></tr> <tr><td>AC</td><td>Q7M316</td><td></td><td></td></tr> <tr><td>DT</td><td>01-MAR-2004 (TREMBUREL. 26, Last sequence update)</td><td></td><td></td></tr> <tr><td>DT</td><td>01-MAR-2004 (TREMBUREL. 26, Last annotation update)</td><td></td><td></td></tr> </table> <p>Query Match 74.7%; Score 61; DB 2; Length 16;    Best local Similarity 73.3%; Pred. No. 0.027;    Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;</p> <p>RESULT 13</p> <table border="0"> <tr><td>Q7M317</td><td>PRELIMINARY;</td><td>PRT;</td><td>16 AA.</td></tr> <tr><td>ID</td><td>Q7M317</td><td>PRT;</td><td>16 AA.</td></tr> <tr><td>AC</td><td>Q7M317;</td><td></td><td></td></tr> <tr><td>DT</td><td>01-MAR-2004 (TREMBUREL. 26, Created)</td><td></td><td></td></tr> <tr><td>DT</td><td>01-MAR-2004 (TREMBUREL. 26, Last sequence update)</td><td></td><td></td></tr> <tr><td>DT</td><td>01-MAR-2004 (TREMBUREL. 26, Last annotation update)</td><td></td><td></td></tr> <tr><td>DE</td><td>Fibrinopeptide A.</td><td></td><td></td></tr> <tr><td>OS</td><td>Ursus sp. (bear).</td><td></td><td></td></tr> <tr><td>OC</td><td>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;</td><td></td><td></td></tr> <tr><td>OC</td><td>Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.</td><td></td><td></td></tr> <tr><td>OX</td><td>NCBI_TaxID=9611;</td><td></td><td></td></tr> <tr><td>RN</td><td>[1]</td><td></td><td></td></tr> <tr><td>RP</td><td>SEQUENCE.</td><td></td><td></td></tr> <tr><td>RA</td><td>Blombaeck B., Blombaeck M., Hann C.;</td><td></td><td></td></tr> <tr><td>RL</td><td>Unpublished results, cited by:</td><td></td><td></td></tr> <tr><td>RL</td><td>Blombaeck B., Blombaeck M.;</td><td></td><td></td></tr> <tr><td>RL</td><td>(In) Hawkes J. G. (eds.);</td><td></td><td></td></tr> <tr><td>RL</td><td>Chemotaxonomy and Serotaxonomy, pp.0.3-20, Academic Press, New York</td><td></td><td></td></tr> <tr><td>RL</td><td>(1968).</td><td></td><td></td></tr> <tr><td>DR</td><td>PIR: G29501; G29501.</td><td></td><td></td></tr> <tr><td>SQ</td><td>SEQUENCE 16 AA; 1622 MW; 09598BB6318BD2C4 CRC64;</td><td></td><td></td></tr> </table> <p>Query Match 73.5%; Score 61; DB 2; Length 16;    Best local Similarity 73.3%; Pred. No. 0.027;    Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;</p> <p>RESULT 14</p> <table border="0"> <tr><td>FIBA_LAMGL</td><td>STANDARD;</td><td>PRT;</td><td>18 AA.</td></tr> <tr><td>ID</td><td>FIBA_LAMGL</td><td>PRT;</td><td>18 AA.</td></tr> <tr><td>AC</td><td>P1454;</td><td></td><td></td></tr> <tr><td>DT</td><td>01-JAN-1990 (Rel. 13, Created)</td><td></td><td></td></tr> <tr><td>DT</td><td>01-JAN-1990 (Rel. 13, Last sequence update)</td><td></td><td></td></tr> <tr><td>DT</td><td>05-JUL-2004 (Rel. 44, Last annotation update)</td><td></td><td></td></tr> <tr><td>DE</td><td>Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).</td><td></td><td></td></tr> <tr><td>GN</td><td>Name=FGA;</td><td></td><td></td></tr> <tr><td>OS</td><td>Lama glama (llama), and</td><td></td><td></td></tr> <tr><td>OS</td><td>Lama vicugna (Vicugna) (Vicugna vicugna).</td><td></td><td></td></tr> <tr><td>OC</td><td>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;</td><td></td><td></td></tr> <tr><td>OC</td><td>Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.</td><td></td><td></td></tr> <tr><td>OX</td><td>NCBI_TaxID=9844, 9843;</td><td></td><td></td></tr> <tr><td>RN</td><td>[1]</td><td></td><td></td></tr> </table>	Q7M316	PRELIMINARY;	PRT;	16 AA.	ID	Q7M316	PRT;	16 AA.	AC	Q7M316			DT	01-MAR-2004 (TREMBUREL. 26, Last sequence update)			DT	01-MAR-2004 (TREMBUREL. 26, Last annotation update)			Q7M317	PRELIMINARY;	PRT;	16 AA.	ID	Q7M317	PRT;	16 AA.	AC	Q7M317;			DT	01-MAR-2004 (TREMBUREL. 26, Created)			DT	01-MAR-2004 (TREMBUREL. 26, Last sequence update)			DT	01-MAR-2004 (TREMBUREL. 26, Last annotation update)			DE	Fibrinopeptide A.			OS	Ursus sp. (bear).			OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			OC	Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.			OX	NCBI_TaxID=9611;			RN	[1]			RP	SEQUENCE.			RA	Blombaeck B., Blombaeck M., Hann C.;			RL	Unpublished results, cited by:			RL	Blombaeck B., Blombaeck M.;			RL	(In) Hawkes J. G. (eds.);			RL	Chemotaxonomy and Serotaxonomy, pp.0.3-20, Academic Press, New York			RL	(1968).			DR	PIR: G29501; G29501.			SQ	SEQUENCE 16 AA; 1622 MW; 09598BB6318BD2C4 CRC64;			FIBA_LAMGL	STANDARD;	PRT;	18 AA.	ID	FIBA_LAMGL	PRT;	18 AA.	AC	P1454;			DT	01-JAN-1990 (Rel. 13, Created)			DT	01-JAN-1990 (Rel. 13, Last sequence update)			DT	05-JUL-2004 (Rel. 44, Last annotation update)			DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).			GN	Name=FGA;			OS	Lama glama (llama), and			OS	Lama vicugna (Vicugna) (Vicugna vicugna).			OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			OC	Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.			OX	NCBI_TaxID=9844, 9843;			RN	[1]		
Q7M316	PRELIMINARY;	PRT;	16 AA.																																																																																																																																																													
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RL	(In) Hawkes J. G. (eds.);																																																																																																																																																															
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DR	PIR: G29501; G29501.																																																																																																																																																															
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DT	05-JUL-2004 (Rel. 44, Last annotation update)																																																																																																																																																															
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).																																																																																																																																																															
GN	Name=FGA;																																																																																																																																																															
OS	Lama glama (llama), and																																																																																																																																																															
OS	Lama vicugna (Vicugna) (Vicugna vicugna).																																																																																																																																																															
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;																																																																																																																																																															
OC	Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.																																																																																																																																																															
OX	NCBI_TaxID=9844, 9843;																																																																																																																																																															
RN	[1]																																																																																																																																																															

RP SEQUENCE.  
 RC SPECIES=L. glama;  
 RA Blomback B.; Blomback M.; Grondahl N.J.;  
 RT "Studies on fibrinopeptides from mammals.";  
 RL Acta Chem. Scand. 19:1789-1791(1965).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=L. vicugna;  
 RA McRob G.A.; Doolittle R.F.;  
 RT "Amino acid sequence studies on artiodactyl fibrinopeptides.";  
 RL Arch. Biochem. Biophys. 122:674-684(1967).  
 CC -!- FUNCTION: Fibrinogen has a double function: Yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.  
 CC -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma) linked to each other by disulfide bonds.  
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.  
 CC Blood coagulation; Direct protein sequencing; Plasma.  
 KW Blood coagulation; Direct protein sequencing; Plasma.  
 FT PEPTIDE 1 18 Fibrinopeptide A.  
 FT NON TER 18 18  
 SQ SEQUENCE 18 AA: 1834 MW: 2444487B8B7F4CC6 CRC64;  
 Query Match 73.5%; Score 61; DB 1; Length 18;  
 Best Local Similarity 73.3%; Pred. No. 0.031;  
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 DSGGDDFLBEGGGVR 16  
 Db 4 DADKGEBFLAEGGGVR 18

RESULT 15

ID	FIBA_CANFA	STANDARD;	PRT;	28 AA.
AC	P02673; P14464;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).			
GN	Name=FGA;			
OS	Canis familiaris (Dog), and			
OS	Vulpes vulpes (Red Fox)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615, 9627;			
RN	[1]			
RP	SEQUENCE.			
RC	SPECIES=C. familiaris;			
RX	REDLINE=76081726; PubMed=1198547;			
RA	Birken S., Wilner G.D., Canfield R.E.;			
RT	"Studies of the structure of canine fibrinogen."			
RL	Thromb. Res. 7:599-610(1975). [2]			
RN	SEQUENCE OF 1-16.			
RC	SPECIES=C. familiaris, and V. vulpes;			
RA	Blomback B., Blomback M., Grondahl N.J.;			
RT	"Studies on fibrinopeptides from mammals."			
RL	Acta Chem. Scand. 19:1789-1791(1965). [3]			
RP	SEQUENCE OF 1-16.			
RC	SPECIES=C. familiaris;			
RX	MEDLINE=66020594; PubMed=5836555;			
RA	Obahr A.J. JR., Colman R.W., Laki K., Gladner J.A.;			
RT	"The nature of the peptide released from canine fibrinogen."			
RL	Biochem. Biophys. Res. Commun. 14:555-558(1964);			
CC	-!- FUNCTION: Fibrinogen has a double function: Yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.			
CC	-!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds.			

CQ -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.

PIR	A94308; A05296.
KW	Blood coagulation; Direct protein sequencing; Phosphorylation; Plasma.
FT	PEPTIDE 1 15 Fibrinopeptide A.
FT	MOD RES 3 Phosphoserine (partial).
FT	CONFICT 2 N -> D (in Ref. 2).
FT	CONFLICT 4 KEGE -> EGKQ (in Ref. 2).
FT	NON TER 28 28 MW: 09DCD3FP923BFEBD2 CRC64;
SQ	SEQUENCE 28 AA: 2958 MW: 09DCD3FP923BFEBD2 CRC64;
Query	2 DSGECDPFLABGGYR 16
Db	2 NSKEGBFIAEQQVR 16

Search completed: January 21, 2005, 08:33:17  
 Job time : 95 secs

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